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MOLECULE TYPE: DNA (recombinant)
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TYPE: nucleic acid
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CURRENT APPLICATION DATA:
double
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STATE: Missouri
    USA
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Sequence 8, Appl.
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-484-274A-17
US-08-391-339-8
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US-08-391-339-7
US-08-391-339-6
US-08-484-274A-6
US-08-391-339-4
US-08-391-339-4
US-08-391-339-37
US-08-391-339-37
US-08-391-339-37
US-08-391-339-37
US-08-391-339-37
US-08-391-339-33
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US-08-484-274A-28
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: GLyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
US-08-997-897-1
US-08-056-200-93
US-08-06-200-93
US-08-0403-378B-14
US-08-258-402-12
US-08-228-402-12
US-08-471-033-18
US-08-471-044-18
US-08-471-046A-18
US-08-471-046A-18
US-08-469-334-18
US-08-469-334-18
US-08-469-334-18
US-08-469-335-US-09-30-529-18
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700 Chesterfield Village Parkway
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 17, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
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GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCCGTCCAAGC
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Best Local Similarity
Matches 1296; Conserv
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; LOCATION: 1..1
US-08-484-274A-17
                                                                                                                                                                                                                                                                STATE: Texas
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US-08-484-274A-17
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Pred. No. 0;
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    Query Match
Best Local Similarity
Matches 1296; Conserv
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                               1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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ZIP: 77210-4433

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Versic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Durkee
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 17, Application US/08484274A Patent No. 5776760 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 17:
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ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. B44F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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Patentin Release #1.0, Version #1.
                                                                                                                           1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                                                                                                                               Score 1288; DI
Pred. No. 0;
0; Mismatches
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STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: HOEFDER, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                         Sequence 8, Application US/08391339
Patent No. 5463175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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US-08-391-339-8
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LENGTH: 1296 base pairs
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FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
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Matches 1291; Conservative
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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STATE: Missouri
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                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38-21 (13560)A
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                1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
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1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA
                                                                                                                                                                                        Tolerant
                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATTERSON, Melinda L.
REGISTRATION NUMBER: 33,062
REFRENCE/POCKET NUMBER: MOBTI30 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713/789-2679
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                    White & Durkee
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                          Sequence 8, Application US/08484274A Patent No. 5776760 GENERAL INFORMATION:
                                                                                                                                                      APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 99.6
Matches 1291; Conservative
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US-08-484-274A-8
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US/08391339

Sequence 7, Application Patent No. 5463175 GENERAL INFORMATION: APPLICANT: Kishore,

Ganesh

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                                                      ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77.7%; Score 1006.4;
86.0%; Pred. No. 0;
ive 0; Mismatches
          TITLE OF INVENTION: Glyphosate Tolerant NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                    38-21(10533)
                                                                                                                                                                                      COMPUTER: IEM PCC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hoerner, Dennis R., Jr. REGISTRATION NUMBER: 30,914
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 38 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (314)537-6099 INFORMATION FOR SEQ ID NO: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
Gerard
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Matches 1115; Conservative
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                                            CORRESPONDENCE ADDRESS:
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STRANDEDNESS:
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.; 0 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/484,274A

07 June 1996 N: 435

FILING DATE:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

COMPUTER READABLE FORM:

COUNTRY: USA 7TP: 77210-4433 Houston

Texas

REFERENCE/DOCKET NUMBER: MOBIL30 38-21(13560)A TELECOMMUNICATION INFORMATION: TELEPHONE: (713)789-2679

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062

DNA (recombinant)

double

STRANDEDNESS:

Linear

MOLECULE TYPE:

SEQUENCE CHARACTERISTICS: LENGTH: 1296 base pairs TYPE: nucleic acid

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INFORMATION FOR SEQ ID NO:
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           CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAGAACGGTCACACCATC
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Patent No. 5776760
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US-08-484-274A-7
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0
 Length 1296
DB 2;
                   181;
Score 1006.4;
Pred. No. 0;
                  0; Mismatches
77.78;
86.08;
        Best Local Similarity 86.0
Matches 1115; Conservative
Query Match
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Tolerant

APPLICANT: Barry, Gerard F. TITLE OF INVENTION: Glyphosate NUMBER OF SEQUENCES: 33 CORRESPONDENCE ADDRESS: APPLICANT: Kishore, Ganesh M. APPLICANT: Barry, Gerard F.

GENERAL INFORMATION:

ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433

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                                      GTGTCTGCTCGTGTTATCGGATTCGAGGCTGAAGGTCGTGCTCTCAAGGGTATCACCACC
                                                                          ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                      1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kishore, Ganesh M.
PAPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                               Score 958.4;
Pred. No. 0;
                                                                                                                                           38-21(10533)
                                                                     US/07/717,370
                                           US/08/156,968
                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (recombinant) US-08-391-339-6
                                                                                                               NAME: Hoerner, Dennis R., Jı
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                               74.0%;
83.7%;
                                                                                                                                                                     TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 6:
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hoerner, Dennis R.,
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 83.7
Matches 1085; Conservative
                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: (FILING DATE:
                                                                  APPLICATION NUMBER:
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FILING DATE:
CLASSIFICATION:
                                                                                   FILING DATE:
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661 GTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTACAACC 720
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                           ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACACTCCAAGTCT
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE

OPERATUR: SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

FILING DATE: 07 June 1996

CLASSIFICATION: 435
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Pla
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADDRESSES:
ATTITE HOUSTON
STREET: P.O. Box 4433
CITY: HOUSTON
STREET: VO. Box 4433
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
RECISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOI
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                                                                                                                                                                 Length 1296;
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                                                                                                                                                                Score 958.4; DB 2;
Pred. No. 0;
0; Mismatches 211;
                                                                                                      (recombinant)
                                                                                                                                                                 74.0%;
83.7%;
(713)789-2679
SEQ ID'NO: 6:
            INFORMATION FOR SEQ ID'NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
                                                                                                                                                                               Best Local Similarity 83.7
Matches 1085; Conservative
                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                     MOLECULE TYPE: DNA
 TELEPHONE:
                                                                                                                    US-08-484-274A-6
                                                                                                                                                                 Query Match
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  Pred. No. 0;
0; Mismatches
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  Best Local Similarity 83.6
Matches 1084; Conservative
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                      GCTACTCCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1...
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08484274A
Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
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NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
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MOLECULE TYPE: DNA (genomic)
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SEQUENCE CHARACTERISTICS:
LENGTH: 1692 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ZIP: 77210-4433
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                                                            GAAGGTGCCTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC
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PatentIn Release #1.0, Version #1.25
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83.6%; Pred. No. 1.4e-298;
ive 0; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                         1380 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1415
                                                                                                                                                                                                          1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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NAME: HOERNEY, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 4:
INFORMATION FOR SEQ ID NO: 4:
LENGTH: 1293 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/391,339
FILING DATE: CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/717,370 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: Patentin Release #1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/08391339 Patent No. 5463175 GENERAL INFORMATION:
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STRANDEDNESS: double
TOPOLOGY: linear
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Matches 1084; Conserv
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NAME: PETLERSON, Mellinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 4:
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Pred. No. 1.4e-298;
0; Mismatches 209;
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FLILNG DATE: 07 June 1996
CLASSIFICATION: 435
                                                                                                                                  ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                                                                                                                                                                                                                                                                             ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                   Sequence 4, Application US/08484274A Patent No. 5776760
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LENGTH: 1293 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Matches 1084; Conservative
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                            541 CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAGAAGGGTCACACCATC
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CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACAACCGCTTTGGT 1257
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                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 71.4%; Score 925.6; DB 1; Best Local Similarity 83.6%; Pred. No. 1.7e-298; Matches 1084; Conservative 0; Mismatches 209;
                                                                                                                                                                             APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                            1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                             1258 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1293
                                                                                                                                                                                                                                                         ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREE: 700 Chesterfield Village Parkway
STREE: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HOEFICH, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 53-6099
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: APPLICATION NUMBER: US/07/717,370
                                                                                                                                    Sequence 3, Application US/08391339
Patent No. 5463175
                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: DNA (genomic)
US-08-391-339-3
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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LENGTH: 1689 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   ZIP: 63198
                                                                                                                    US-08-391-339-3
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                            PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (synthetic)
US-08-484-274A-27
                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                           TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.5%;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
           STATE: Texas
COUNTRY: USA
ZIP: 77210-433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 4.5
Best Local Similarity 96.8
Matches 60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
Houston
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TOPOLOGY: 11n
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US-08-391-339-30
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Pred. No. 1.9e-10;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                               APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                       ADDRESSEE: Monsanto Co. BB4F
ADDRESSEE: Monsanto Co. BB4F
STREFF: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,914
ER: 38-21(10533)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILLING DATE:
APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(1
TELECOMMUNICATION INFORMATION:
FELEPHONE: (314,537-6099
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                        Sequence 27, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-27
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Best Local Similarity 96.8%;
Matches 60; Conservative C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                              US-08-391-339-27
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SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, malinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MGFT130 38-21(13560)A
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
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Pred. No. 1.9e-10;
0; Mismatches 2;
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Patent No. 5463175
GENERAL INFORMATION
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
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ATTORNEY/AGENT INFORMATION:
NAME: HOGERER, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/POCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: Ilnear
MOLECULE TYPE: DNA (synthetic)
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62 AAATCACT 69
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Search completed: January 1, 2001, 03:19:01 Job time: 29365 sec

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January 1, 2001, 03:16:17; Search time 7299.04 Seconds (Without alignments) 775.497 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                               OM nucleic - nucleic search, using sw model
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1296
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Maximum DB seq length: 2000000000
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gb_pr4:*
gb_htg3:*
gb_htg6:*
gb_htg5:*
gb_htg7:*
em_htg1:*
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Perfect score:
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em_htg20:* em_htg21:*

em_htg17: em_htg18: em_htg19:

em_htg14: 'em_htg15: 'em_htg16: 'em_htg16:

em_htg12: em_htg13:

9b_pr6:* 9b_pr7:* 9b_htg20:* gb_htg21:* gb_htg22:* gb_htg23:*

gb_ro:*
gb_sts1:*
gb_sts2:*
gb_sy:*

gb_un:* gb_vil:* gb_vi2:*

9b_1n3:*
9b_htg15:*
9b_htg15:*
9b_htg17:*
9b_htg17:*
em_htg4:*
em_htg4:*
em_htg6:*
9b_htg19:*
em_htg8:*
em_htg8:*
em_htg9:*
em_htg9:*
em_htg10:*

44444446555 44444446555 4444446555 444446555 44444655 444465 44465 4444

em_hum5: *
9D_p13: *
9D_p15: *
9D_ht98: *
9D_ht99: *
9D_ht910: *
9D_ht910: *
9D_ht910: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	AR016604 Sequence	I15337 Sequence 17	AR016595 Sequence	I15328 Sequence 8	A59869 Sequence 1	AR016594 Sequence	Il5327 Sequence 7	AR016593 Sequence	I15326 Sequence 6	AR016591 Sequence	AR016592 Sequence	I15325 Sequence 4
		(016604	115337	1016595	5328	69869	101.6594	5327	(016593	5326	(016591	1016592	5325
	ID	A	Ξ	AF	Π	A	AF	Ξ	AF	Ξ	AF	ΑF	Ξ
	DB		Ŋ	'n	S	5	'n	S	Ŋ	S	S	ß	S
	Query Match Length DB	1296	1296	1296	1296	1631	1296	1296	1296	1296	1692	1293	1293
æ	Query Match	100.0	100.0	99.4	99.4	95.6	77.7	7.77	74.0	74.0	73.8	71.4	71.4
	Score	1296	1296	1288	1288	1200.4	1006.4	1006.4	958.4	958.4	926.8	925.6	925.6
	Result No.	1	7	r	4	S	9	7	80	6	10	11	12

Db 121 GAAGGTGCCTCTTTCGGTAACGCTTCCAAGTG Oy	Qy 661 GTGTCTGCTCGTGTTATCGGATTCGAGACTGAA Db 661 GTGTCTGCTCGTGTTATCGGATTCGAGACTGAA Qy 721 ACCAACGGTGTTATCGGATTCGAGCTGTTGTGTGTGTGTG	Oy 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTAC Db 1021 GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTAC OY 1081 ATCCCGGATTCCCTTCCAGTGATTGCTGGTGCT
115324 Sequence 3 M69158 Pseudomonas AR016613 Sequence 115345 Sequence 27 AR016616 Sequence 30 AR016619 Sequence 31 AR016619 Sequence 31 AR016619 Sequence 32 AR016618 Sequence 32 AR016618 Sequence 31 AR016617 Sequence 31 AR016614 Sequence 31 AR016614 Sequence 31 AR016619 Sequence 31 AR016619 Sequence 32 AR016619 Sequence 32 AR016619 Sequence 31 AR016619 Sequence 31 AR016619 Sequence 31 AR016619 Sequence 31 AR01619 Sequence 31 AR01619 Sequence 31 AR01619 AS Sequence 31 AR017619 AND MAS	. PAI	0%; Score 1296; DB 5; Length 1296; 0%; Pred. No. 0; 0; Mismatches 0; Indels 0; Gaps 0; GGTTGGTATCCTGGAGTTGGTTTGCACT 60
13 925.6 71.4 1689 5 115324 14 64.6 5.0 3430 2 PSEAKSD 15 58.8 4.5 62 5 AR016613 17 58.4 4.5 69 5 AR016616 18 58.4 4.5 69 5 AR016616 20 56.2 4.3 69 5 115349 21 53.6 4.1 68 5 115352 22 53.6 4.1 68 5 AR016618 23 53.4 4.1 68 5 AR016617 24 53.8 4.1 61 5 AR016617 25 52.8 4.1 61 5 AR016617 26 52.8 4.1 65 5 AR016617 27 50.2 3.9 7334 11 AF056191 28 50.3 3.9 2289 2 PSEKSDA 30 49.8 3.8 232361 29 AE003724 31 46.4 3.6 209973 57 AC073755 25 56 46 3.5 1596 88 MM070654 26 57 46 3.5 1596 88 MM070654 27 60.4 3.8 186935 48 AC023222 28 44.8 3.5 1269 88 MM070654 29 44.8 3.5 128469 56 AC013022 20 44.8 3.5 186935 48 AC023222 21 42.8 3.3 186935 48 AC02322 22 42.8 3.3 186935 48 AC023222 23 42.6 3.3 11343 88 MMCAPSI	RESULT 1 ARO16604 1296 bp DNA LOCUS DECUS ARO16604 1 2196 bp DNA ARO16604 VERSION ARO16604 1 G1:3972881 CUROWN REVERS SOURCE Unclassified. DECUS REFERENCE 1 (bases 1 to 1296) AUTHORS BARY, G. Francis and Kishore, G.Murthy TITLE JOURNAL Glyphosate tolerant plants JOURNAL Glyphosate folerant plants JOURNAL GLYPHOSATE JOURNAL GLY	Query Match Dest Local Similarity 100.0%; Score 1296; Dest Local Similarity 100.0%; Pred. No. 0; Matches 1296; Conservative 0; Mismatches Oy 1 ATGGCTGAGAACCACAAGAAGGTTGGTATCGCTGGAGC Oy 61 GCTTTGATGCTTCAAGGTTGGATTCAAGGTTACCTT Op 61 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTT Oy 62 GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTT Oy 7121 GAAGGTGCTTCAACGTGTGATCAAGGTTACCTT Oy 121 GAAGGTGCTTCAACGTGATGCATCAAGGTTACCTT Oy 121 GAAGGTGCTTTCGGTAACGTTGAAGGTTACCTT

1080 1140 TCTACACTCGGGCTCGTAAGTTGCTTCCA 1020 1080 480 480 780 900 CTCCAATGACCGCAACCCTCGTTTCTGAG 1200 CTCCAATGACCGCAACCCTCGTTTCTGAG 1200 420 720 720 240 240 420 540 540 840 840 096 960 300 300 360 360 900 099 999 780 900 TCAACGGTTCCTCCGTTGTTCCAATGTCC 180 900 CTTGGTTGATTCGTTTGTTTGCTTGCTGGA TCCTTATCGAAGAGAACGGTCACCATC AAGGTCGTCTCAAGGGTATCACCACC TTGTTGCAGCTGGTGCACACTCCAAGTCT GCTGGAACCGTTGAGTTCGCTGGTCTCACT ACTCCAAGTGGATGGGTTTCCGTCCAAGC TCAGCGCTGATGCGTTGCGTGATTTCGAT CGTCGTTTCATCGCTAACGGTGGAGAGTTC CAACTACCGATGCTTCTGGAAAGTTCATC CACTCCGTAACCTCATCAAGTCCACTGTG TGGATACCGAACGTGGATACCACATCGTG CAACTACCGATGCTTCTGGAAAGTTCATC CTTGGTTGATTCGTTTCTTGCTTGCTGGA ATGCTAGCCACCTTATCCGTCACGAAGGT TCGCCAGGGACCGTGGAGGTTGGGAACTT TTGTTGCAGCTGGTGCACACTCCAAGTCT CTACCCGTACTCCAGACGTTATCTACGCT

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AACCCACAAGGTCTCGTGACTCTCTTGTTTTCGTCGTTTTCATCGCTAACGGTGGAGAGTTC
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Pred. No. 0;
0; Mismatches
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Barry, G.Francis and Kishore, G.Murthy.
Glyphosate tolerant plants
Patent: US 5776760-A 8 07-JUL-1998;
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants.
Patent: US 5463175-A 17 31-CT-1995;
Location/Qualifiers
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Pred. No. 0;
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/organism="Arabidopsis
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Location/Qualifiers
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241 ATCGGTTTCGGCTACTTTCCAACCATCATGCTTGGTTGGT	Db 841 ATGGGAATCCGGAAGCCGTTCGACGACGACGATCGGAAATTCATC 900 Oy 901 GCTACTCCTATGGACATGGCTTTCGTGTACCTTGAGTTTCGTGGTACTTCACT 960 I 901 GCTACTCCTATGGACATGGGTCTTCGTGTACTTGAGTTTCGTGGTCTCACT 960 Oy 901 GCTGCTCCTATGGAATGGGTCTTCGTGTTGCTGGTTTGCTGGTCTCACA 960 Oy 901 GCTGCTCCTAACTGGAAGGGTCTTCTTACACTTGCTGGTTTCCTTCACA 960 Oy 1021 GCTGCTCTCTAACTGGAAGGGTCTTCTTATACGCACGCTCGAAACTTTCTTCA 1020 Oy 1021 GCTCTCGCTCTAACTGGAAAGGTGTTTTCCAAGTTGGTTTCCAAGC 1080 I 1
	REPERENCE L(bases 1 to 1296)

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   ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCT
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Barry, G. Francis and Kishore, G. Murthy, Glyphosate tolerant plants
Patent: US 5776/60-A 6 07-JUL-1998;
Location/Qualifiers
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Sequence 6 from patent US 5'
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Pred. No. 1e-273;
0; Mismatches 181;
                                                                                         Unclassified.

1 (bases 1 to 1296)
Barry, G.F. and Kishore, G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 7 31-OCT-1995;
Location/Qualifiers
                               5463175
                                                                                                                                                                /organism="unknown"
344 c 332 g
                               Sequence 7 from patent US
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86.08;
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4e-260;
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                                  1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                          Score 958.4; Di
Pred. No. 4e-26
0; Mismatches
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Barry, G.F. and Kishore, G.M.
Glyphosate tolerant plants.
Patent: US 5463175-A 6 31-OCT-1995;
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                                                                                         II5326 1296 bp DNA
Sequence 6 from patent US 5463175.
II5326
II5326.1 GI:1250234
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Best Local Similarity 83.7%;
Matches 1085; Conservative (
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AUTHORS
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FEATURES
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Matches 1084;
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                                                   ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACCTCCAAGTCT
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No. 1.1e-259;
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Barry,G.Francis and Kishore,G.Murthy
Glyphosate tolerant plants
Patent: US 5776/50-A 3 07-JUL-1998;
Location/Qualifiers
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Sequence 3 from patent AR016591 GI:3972868
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                                                        ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGCTGCTCCACCTCCAAGTCT
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 3463175-A 4 31-OCT-1995;
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I15325.1 GI:1250233
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Pred. No. 7.6e-251;
); Mismatches 209;
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Barry,G.Francis and Kishore,G.Murthy.
Glyphosate tolerant plants
Patent: US 5776760-A 4 07-JUL-1998;
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Sequence 4 from patent US 5776760.
AR016592
AR016592.1 GI:3972869
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 GCGACACCTATGGAAATGGGGCTTTCCCCTTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA
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Pred. No. 7.6e-251;
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Sequence 3 from patent US 5463175.
I15324 II:1250232
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                                                             Length
                                                                              Indels
                                                           Score 925.6; DB 5;
Pred. No. 7.6e-251;
); Mismatches 209;
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                          281
Location/Qualifiers
1. .1293
                 /organism="unknown"
367 c 359 g
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                                                            71.4%;
83.6%;
                                                                               Conservative
                                                                     Similarity
                                                                              Matches 1084;
                                                            Query Match
                                                                      Best Local
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Gaps 9

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                                                                CGTCGTCTCAACGGTGTTCGTACTCAAATCCTCAGCGCTGATGCGTTGCGTGATTTCGAT
                                                                                                CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAAGGGTCACACCATC
                                                                                                                                                                                         GTGTCTGCTCTGTTATCGGATTCGAGGCTGAAGGTCGTGCTCTCAAGGGTATCACCACC
                                                                                                                                                                                                 ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCT
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                                                                                                                                                        AACCCACAAGGTCTCGTGACTCTCTTGTTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC
                        CCTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT
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PSEAKSD 3430 bp DNA BCT 26-APR-1993 Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase gene, complete cds.

DEFINITION

14

RESULT COCUS

PSEAKSD

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/product="ketoglutarate semialdehyde dehydrogenase"
/product="ketoglutarate semialdehyde dehydrogenase"
/protein_id="naAa25698.1"
/db_xref="Gi1150982"
/db_xref="Gi1150982"
/translation="writTreorace"
/translation="writTreorace
                                                                                                                                                                                   1 (bases 1 to 3430)
Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
Nucleotide sequences of hydroxyproline specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2214 TGGTGGGCGCGGGATTGTCGCCTTGCCTGCAACTGGCCCGCCAGGCCTTC 2273
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                                                                                                                           gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 AGGTTACCTTGATTGATCCAAACCCAGGTGAAGGTGCCTCTTTCGGTAACGCTGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="ketoglutarate semialdehyde dehydrogenase"
603. .2180
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/gene="ketoglutarate semialdehyde dehydrogenase"
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Pred. No. 3.1e-07;
                             ketoglutarate semialdehyde dehydrogenase
Pseudomonas putida DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pseudomonas putida
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                                                                                                                                                                                                                                                                                                    putida
Unpublished (1991)
Location/Qualifiers
1. .3430
1. .***em="Pseudomon?"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:303"
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                                                                                                                           Bacteria; Proteobacteria;
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Best Local Similarity 47.4%;
Matches 193; Conservative (
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GI:150981
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                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
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05-DEC-1998
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4.5%; Score 58.8; DB 5; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.4e-05;
Matches 60; Conservative 0; Mismatches 2; Indels
                                   PAT
                                                                                     Unknown.
SM Unknown.
Unclassified.
ACE 1 (bases 1 to 62)
IORS Barry, G.Francis and Klahore, G.Murthy.
LE Glyphosate tolerant plants
JRNAL Patent: US 5776760-A 27 07-JUL-1998;
Location/Qualifiers
1. 62
'Arqanism="unknown"
                              AR016613 62 bp DNA
Sequence 27 from patent US 5776760.
AR016613.1 GI:3972890
RESULT 15
ARO16613
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
FEATURES
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cDNA sequence of a cDNA sequence of PMouse SRY-related
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T33007
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X87940
V64558
V44449
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Z22301
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A34791
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ID Q20835 standard; DNA; 1296 BP
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P-PSDB; R20642.
  24-JUN-1991;
25-JUN-1990;
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1 ATGGCTGAGAACCAAGAA......AAACTGGTCCTGCATCCTAA 1296
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                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                480022 seqs, 187831343 residues
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                                                                                                                                     January 1, 2001, 03:45:17
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Maximum Match 100%
Listing first 45 summaries
                                                                                              - nucleic search, using sw model
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T85664
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Score

Result . 2

The sequence is that of the gene encoding a glyphosate oxidoreductase (GON) enzyme, the gene sequence was synthesised so that it could be redesigned to eliminate as much as possible the following sequences or redesigned to eliminate as much as possible the following sequences or redesigned to eliminate avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more; A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently corrected in plant genes. The G + CA for the synthetic gene is 51% and the potential to form short, high energy, hair-pin structures is cauced. However it still encodes the wild type GOR enzyme. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant.

Transformed plants resistant to glyphosate can be obtd: so that weeds can be selectively controlled in fields contg. crops. ; 0 180 240 240 300 360 360 420 480 540 009 300 420 480 9 Gaps 1 ATGGTTGAGAACCACAAGAAGGTTGGTATCGCTGGAGCTTGGAATCGTTGGTGTTTGCACT 181 atgccaggaaacttgactagcgttccaaagtggcttcttgacccaatgggtccattgtcc AGACCAAACAAGGTGAAGGAAGCTAAGGCTAAGGCAAACCTCGTCATCAAGTCCACTGTG agaccaaacaaggtgaaggagcaagctaaggcactccgtaacctcatcaagtccactgtg CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAGGGACCGTGGAGGTTGGGAACTT cgtcgtctcaacggtgttcgtactcaaatcctcagcgctgatgcattgcgtgatttcgat cctaacttgtctcacgcctttaccaagggaatccttatcgaagagaacggtcacaccatc ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC CCTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT CGTCGTCTCAACGGTGTTCGTACTCAAATCCTCAGCGCTGATGCATTGCGTGATTTCGAT CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAGGAACGGTCACACATC ; 0 DB 13; Length 1296; transform plants to produce plants tolerant to glyphosate herbicide Indels Sequence 1296 BP; 271 A; 359 C; 305 G; 361 T; 0 other; 5, 0; Mismatches Score 1288; Pred. No. 0; Claim 1; Page 1032; 142pp; English See also Q20832-Q20841 and Q22705 99.4%; Best Local Similarity 99.6 Matches 1291; Conservative Query Match 61 301 61 181 301 361 361 421 421 481 541 481 g õ q ò QQ Ор qq qq g ò qq ò ç ò ò ò QQ ò g

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                                   CTTGCTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTG
                                                                      GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGGTTTCCGTCCAAGC
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                          ACCAACGGTGTTCTTGCTTGTTGCAGCTGTTGTTGCAGCTGGTTGCACACTCCAAGTCT
                                                                                                                                                                                                                   Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plan 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herk tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
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) NOVARTIS-ERFINDUNGEN VERW GES
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                                                                                   mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
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                                                        This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium
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Pred. No. 0;
                    transgenic sugar
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sequence 1;
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                                                                                                                                                                                                                   ctcctcgcaggtgagaagacctctatcgacatctcccattcgcaccaaaccgtttcggt
TTCGGTCACGGTCACCTCGGTATGACTGGTGCTCCAATGACCGCAACCCTCGTTTCTGAG
                                                                                                                                         CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAAACCGTTTCGGT
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                                     1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
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ogotgatgcattgcgtgatttcgatcctaacttgtctcacgcctttaccaagggaatcct 873

Page

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Inducible promoter linked to a gene (1) that confers resistance to a finducible promoter linked to a gene (1) that confers resistance to a funducible promoter linked to a gene (1) that confers resistance to a bycline (glyphosate) or its salts, but may also be a gene for resistance to a lycine (glyphosate) or its salts, but may also be a gene for resistance to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolones, confer the inducible promoter (e.g. alch, alck, alck, aldh or other alck-induced gene promoter) is operatively linked to an alc aldh or other alck-induced capression of (1) avoids the risk that constitutive expression in all interfere with plant development; allows volunteer plants to be controlled by herbicide applied without inducer and minimises the chance that herbicide resistant strains of weeds will arise. The expression cassette is strictly controlled and suitable for general use in plants (both mono- and dicotyledons). The alchale for general use in plants (both mono- and dicotyledons). The alchale for general use sometitutive expression of glyphosate oxides (GPX) in plants.

Switchable GOX was expressed alone or in conjunction with constitutive expression of 5-enol-pyruvylshikimate 3-phosphate (BPSPS) CP4. Constructs were optimised for expression in mono- and dicotyledonous crop species. The present sequence comprises a fusion of the GOX gene fused to the chloroplast transit sequence a from Arabidopsis RUBISCO (CPTI). This
   glyphosate, avoids constitutive expression and minimises development of herbicide tolerant weeds
                                                                                      59pp; English.
                           herbicide tolerant weeds
                                                                                Example 3; Fig 7;
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Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

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                                  1 ATGCCTGAGAACCACAAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTTGCACT
                                         394 gaaggigettettteggtaaegetggitgetteaaeggiteeteegtigiteeaaigtee
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                                                                                                                                                                       -----CAATGGGTCCATGTCCATCGGTTTCGGCTACTTTCCAACCATCATGCCTTG
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                                                                                                                                                                                                                                                                                                                                                        DB 18; Length 1631;
                  50;
                 16; Indels
 Score 1200.4;
        Pred. No. 0;
0; Mismatches
Query Match
Best Local Similarity 95.1%;
Matches 1280; Conservative
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/*tag= a
/note= "encodes wild type glyphosate oxidoreductase"
934 tttcatcgctaacggtggagagttcgtgtctgctcgtgttatcggattcgagactgaagg
                                                                                                                                                                                                                                                           GTCACCTCGGTATGACTGGTGCTCCAATGACCGCAACCCTCGTTTCTGAGCTCCTCGCAG
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                                        TITCATCGCTAACGGTGGAGAGTTCGTGTCTGCTCGTGTTATCGGATTCGAGGG
                                                                                 TCGTGCTCTCAAGGGTATCACCACCACCAACGGTGTTCTTGCTGTTGATG------
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                                                                                                                                                                 CCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCCAACC
                                                                                                                                                                                                         CAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACTCCTA
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9..1304
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It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant.
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                                                                                                                                                                                                     Gene encoding glyphosate oxido-reductase enzyme - used to
transform plants to produce plants tolerant to glyphosate
herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
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Pred. No. 0;
0; Mismatches
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86.08;
                                                                                     91US-0717370, 90US-0543236,
                                                             91WO-US04514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 1114; Conservative
                                                                                                                                                     Kishore GM, Barry GF;
                                                                                                                            (MONS ) MONSANTO CO.
                                                                                                                                                                            WPI; 1992-041559/05.
P-PSDB; R20642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                             24-JUN-1991;
                                                                                                 25-JUN-1990;
            WO9200377-A
                                     09-JAN-1992
                                                                                      24-JUN-1991
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                                   actaacogtgttctggctgttgatgcagctgttgttgcagctggtgcacactctaaatca
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                        CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAGGGACCGTGGAGGTTGGGGAACTT
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                                     Location/Qualifiers
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/*tag= a
/note= "encodes wild type glyphosate oxidoreductase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.8%; Score 956.8; DB 13; Length 1321; 83.6%; Pred. No. 2.1e-289; ive 0; Mismatches 212; Indels 0;
                                                                                                                                                                                                                                              Gene encoding glyphosate oxido-reductase enzyme - used to
transform plants to produce plants tolerant to glyphosate
herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1321 BP; 292 A; 373 C; 369 G; 287 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                  also Q20832-Q20841 and Q22705
Recombinant; GOR; resistance; ss
                                                                                                                                                                                                                                                                                              Claim 1; Fig 3; 142pp; English.
                                                                                                                                                    91US-0717370
90US-0543236
                                                                                                                                 91WO-US04514
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 83.6
Matches 1084; Conservative
                   Bacterial isolate LBAA.
                                                                                                                                                                                                       Kishore GM, Barry GF;
                                                                                                                                                                                                                         WPI; 1992-041559/05.
P-PSDB; R20642.
                                                                                                                                                                                  (MONS ) MONSANTO CO.
                                                                                                                                 24-JUN-1991;
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25-JUN-1990;
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                                       CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAGGGACCGTGGAGGTTGGGAACTT
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                                                                                'note = "glyphosate oxidoreductase coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 953.6; DB 13; Length 1692;
Pred. No. 2.4e-288;
0; Mismatches 214; Indels 0;
                                                                                                                                   /*tag= c
/note= "not present in alternative sequence"
                                                                                                                                                                 /*tag= d
/note= "not present in alternative sequence"
                                                                                                                                                                                                                                                                                                                                                                  Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1692 BP; 381 A; 478 C; 471 G; 361 T; 1 other;
                                                                                                                present in alternative
                                                  Location/Qualifiers
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         Recombinant; GOR; resistance;
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83.5%;
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/note= '
                                                                        *tag=
                             Bacterial isolate LBAA
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                                                                                         misc_feature
                                                                                                                         misc_feature
                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                        24-JUN-1991;
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25-JUN-1990;
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atogogaatcoggaagcogotcoacgoattocgacgaccgatgcgtcaggaaaattcatg 1019
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CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAGGGACCGTGGAGGTTGGGAACTT
                                                                                                                                                                               catctgaccgtatatcgtggagaagcagacttcgccaaggaccgcggaggttgggaactg
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                                                         CCTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT
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/note= "glyphosate oxidoreductase coding region"
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                                                                                                                            Recombinant; GOR; resistance; ss
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Score 922.4; Pred. No. 1.4

Query Match
Best Local Similarity 83.5%;
Matches 1082; Conservative

ATGCCTGAGAACCACAAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTTTTGCACT

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                                                           CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAAACCGTTTCGGT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvylshikimate-3-phosphate synchase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capa of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
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                                                                                                                                                                                                                                                       Sugar beet, transformation, T-DNA; insertion, cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
                    TTCGGTCACGGTCACCTCGGTATGACTGGTGCTCCAATGACCGCAACCCTCGTTTCTGAG
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                                                                        CCTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT
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                                                                                                                                                 This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as
                                                                                                                                                                                                                                                                                                                                                                                               7384
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                                                                                                                                                                                                                                                                                                     1 ATGCCTGAGAACCACAAGATGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTTGCACT
                                                                                                                                                                                                                                                                                                                                                                                      7325 gaaggtgcttcttccggtaacgctggttgcttcaacggttcctccgttgttccaatgtcc
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                                                                                                                                                                                                                                                                                                                                                                             GAAGGTGCCTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC
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                                                                                                                                                                                                                                                                 DB 20; Length 8798;
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0
                                                                                                                                                                                                                                    Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;
                                                                                                                                                                                                                                                                                   Indels
                                                                                                               Glyphosate resistant transgenic sugar beet plants
                                                                                                                                                                                                                                                                Match 68.8%; Score 892.2; DB 20
Local Similarity 99.7%; Pred. No. 9.6e-269;
les 894; Conservative 0; Mismatches 3;
                                                       MBH.
                                             (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES
                                                                          Tenning PP;
                                                                                                                                Claim 11; Page 31-36; 55pp; English
                           97US-0112003
                                                                          Steen P,
                                                                                           WPI; 1999-313347/26
                                                                          Mannerloef M,
                           31-OCT-1997;
        29-OCT-1998;
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Matches
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This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein 1V, ORF66, ORF67 which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF99, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D, ORF73 which encodes immediate early protein (IPP), K14 which encodes CX-2 (v-adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein. K15. KSIW is a new human Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neoplasm occurring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-: dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHV8; capsid protein IV; tegument protein IV; glycoprotein; kaposin; cyclin D; immediate early protein; IEB; OX-2; v-adh; G-protein coupled receptor; FGARAT; ds.
7985 cttgctaactcccttggtgatgacatcccattggataccgaacgtggataccacatcgtg 8044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8101
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                                                                                                                                      7865 gtgtctgctgtgttatcggattcgagactgaaggtcgtgctctcaagggtatcaccacc
                                                                                                                                                                                                                                                                          721 ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCT
                                                                                                                                                                                                                                                                                                                                                                             781 CTTGCTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATGGTG
                                                                                                   GTGTCTGGTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                    - encodes
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di.hydro:folate reductase and is useful for treatment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSHV LUR DNA (nucleotides 105,301-137,507).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaposi's sarcoma-associated herpesvirus
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V73805
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Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma;
lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides;
HIV immune status; anti-inflammatory agent; therapy; ds.
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                                                                                                                                    727 GGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCTCTTGCT 786
                                                                                                                                                                                                               787 AACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCC 846
                                                                                                Gaps
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                                                                                                                                                                                                                                                                                         847 AACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACT
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                                                          Length 32207;
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Sequence 32207 BP; 7229 A; 9156 C; 8713 G; 7109 T; 0 other;
                                                                                                Indels
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                                                        Score 39.8; DB 20;
Pred. No. 0.11;
0; Mismatches 127;
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/product= glycoprotein M
complement (69412..69915)
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                                                          3.18;
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                                                        Query Match 3.19
Best Local Similarity 47.79
Matches 116; Conservative
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This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known as herpes virus (HHVB). This sequence contains the DNAs of the cas human herpes virus (HHVB). This sequence contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral macrophage inflammatory protein (MIP) II; (b) viral interleukin-6 (IL-6); (c) viral kRF I; (d) complement-binding protein; glycoproteins B, Mor L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by it, and antibodies (Ab) specific for the proteins are useful for conceding allive, specifically for diagnosis of Kaposi's sarcoma, in body fluids or tissue samples. HHVB infections can be treated with antisense or triplex forming molecules or agents that bind specifically to the protein can be used in protective vaccines. Ab may also be used in the protein can be used in protective vaccines. Ab may also be used to the protein can be used in protective vaccines. Ab may also be used in the protein many many be used in many be implicated in many contains and the many many cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e.g. treating rheumatoid arthritis. This sequence is stated as containing \mathbf{81} open reading frames.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other lymphoproliferative diseases such as lymphomas, leukaemia, splenomegaly and mycosis fungoides. Cells and animals containing the nucleic acid are useful for drug screening. HHVB derived peptides can be used as targets for antiviral drugs, e.g. dihydrofolate reductase gene can be inhibited with methotreate. These can also be used to determine the immune status of a patient infected with HIV. HHVB derived protein viral MIP III may be used as an anti-inflammatory agent for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                virus
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                                                                                                                                         /product interferon regulatory factor 3 90173..90643 /*tag k
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                                                    interferon regulatory factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (111931..112443)
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96US-0686243.
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96US-0686350.
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96US-0708678
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960S-0747887.
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/product 1
39600
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13-NOV-1996;
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966 TCCTAAC 972
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                                                            125202 catcctgctgctgctcatcctgctgctgctcatcctgctgctgctgctgctgctgctgctgct 125261
                                                                                                                                                                    The invention relates to the diagnosis of spinocerebellar ataxia type III (SCAIII) syndrome using reverse dot hybridisation or PCR-microplate hybridisation (PCR-MPH). The method comprises attaching a potion of the
                                                                                      846
                                                                                                                        906
                                                   GGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGCTGCACACTCCAAGTCTCTTGCT 786
                                   Gaps
                                                                                                                                                                                                                                                                                                                               Spinocerebellar ataxia type III; SCAIII; reverse dot hybridisation; PCR-microplate hybridisation; PCR-MPH; trinucleotide repeat; TNR;
                                                                                      787 AACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCC
                                                                                                                                  847 AACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACT
                                                                                                                                                           CCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACTGCTGCT
              Length 137507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosis of spinocerebellar ataxia type III (SCA III) syndrome using techniques which ensure highly accurate diagnosis
                                  Indels
                                                                                                                                                                                                                                                                                                               Spinocerebellar ataxia type III (SCAIII) gene fragment.
                                 0; Mismatches 127;
                DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "trinucleotide repeat"
              Score 39.8;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
137..355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 12-13; 28pp; English.
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(SMSU ) SAMSUNG FINE CHEM CO LTD.
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                                                                                                                                                                                                                                                          X89891 standard; DNA; 397
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137..139
                                  Conservative
                                                                                                                                                                                                                                                                                                                                                SCAIII syndrome; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-527634/44.
                         Similarity
                                                                                                                                                                                                             Db 125382 cat 125384
                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                             repeat_unit
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                                116;
                Query Match
                         Best Local
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SCAIII gene containing 73 copies of the trinucleotide (CAG) repeat unit (the present sequence) to a substrate, and hybridising with amplified testee genomic DNA containing copies of the trinucleotide units, PCR amplified with labeled primers (XB989-90). The new method is useful for diagnosis of SCAIII syndrome, and for determining the severity of the disease. The present sequence represents the SCAIII gene fragment containing 73 trinucleotide (TNR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 786 TAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       726 CGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGCTGCACACTCCAAGTCTCTTGC 785
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; PCTC4 region; X chromosome; q13 region; polymorphism;
mental retardation; autism; depression; bipolar affective disorder;
hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents the cDNA sequence of the murine OPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       846 CAACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    906 TCCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACTGCTGC
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                                                                                                                                                                                                                                                                                                                                                    Length 397;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                      Sequence 397 BP; 124 A; 104 C; 104 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                 Score 37.4; DB 20;
Pred. No. 0.063;
0; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USSH ) US DEPT HEALTH & HUMAN SERVICES. (IOWA ) UNIV IOWA RES FOUND.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequence of a murine OPA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP.
                                                                                                                                                                                                                                                                                                                                                 Query Match 2.9%;
Best Local Similarity 47.0%;
Matches 116; Conservative
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245602 standard; cDNA; 6558
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us-08-484-274-17.rng

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gene. The human OPA gene is derived from the PCTG4 region of chromosome Xq13. Polymorphisms in this region are associated with mental retardation, autism, depression, bipolar affective disorder or hypothyroidism. One 12 bp insertion polymorphism occurs within the coding region of the human OPA gene, and introduces a 4 amino acid insertion in a putative OPA domain. This domain has been shown to be involved in tissue specific expression. Another polymorphism consists of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp polymorphism. Another polymorphisms consists of a dinucleotide repeat approximately 7 kb upstream of the 12 bp polymorphism. The specification describes a method for screening for polymorphisms in a PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related sequences within the q13 region of the X chromosome have polymorphisms to associated with neuropsychiatric disorders. The methods can be used to screen for the presence of a heritably linked form of mental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGCTGCTGCTGTTGCTGTTGCTGCTGTTGCCGTAGCATCTGCTGCTGCTGCTGTTG 6217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               845 CCAACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTA 904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     665 CTGCTCGTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACCACCACCA 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; PCTG4 region; X chromosome; q13 region; polymorphism;
mental retardation: autism; depression; bipolar affective disorder;
hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              725 ACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACCTCCAAGTCTCTTG
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0
                                                                                                                                                                                                                                                                                                                                                                                                 Length 6558;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                             Score 35.6; DB 21;
Pred. No. 1;
0; Mismatches 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                              / Match 2.7%; Sco
Local Similarity 45.2%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA sequence of human OPA gene.
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                                                                                                                                                                                                                                                                                                     hypothyroldism.
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The present sequence represents the CDNA sequence of the human OPA gene, which is derived from the human PCTG4 region of chromosome Xq13.

Polymorphism in this region are associated with mental retardation, autism, depression, bipolar affective disorder or hypothyroldism.

Cone 12 bp insertion polymorphism occurs within the coding region of the human OPA gene, and introduces a 4 amino acid insertion in a putative OPA domain. This domain has been shown to be involved in tissue specific expression. Another polymorphism consists of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp polymorphism. Another polymorphisms on the 12 bp polymorphism. Another polymorphism. The specification describes a method for screening for polymorphisms in a PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related sequences within the q13 region of the X chromosome have polymorphisms associated with the q13 region of the X chromosome have polymorphisms associated with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; SRY; primer; PCR; polymerase chain reaction; amplification; probe;
HMG box; human; bovine; sex; animal; birth; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          643 GCTAACGGTGGAGAGTTCGTGTCTGCTCGTGTTATCGCATTCGAGACTGAAGGTCGTGCT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                            neuropsychiatric disorders. The methods can be used to screen for presence of a heritably linked form of mental retardation, autism, depression, bipolar affective disorder or hypothyroldism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6289 GCTGCTGCCGCAGGATCTGCTGCTGCTGCTGCCGGATGTGGTACTGCTGCTGCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 CTCAAGGGTATCACCACCACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of polymorphisms in the PCTG4 region of Xq13 for diagnosing mental retardation or autism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6794 BP; 1624 A; 1938 C; 1754 G; 1478 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.7%; Score 35.2; DB 21; Best Local Similarity 54.7%; Pred. No. 1.4; Matches 70; Conservative 0; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product = SRY-related protein
                                                                                                                                Example 7; Page 68-71; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
7148..8335
/*tag* a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T333007/c
ID T33007 standard; DNA; 10266 BP.
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    Ginns EI;
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                                      WPI; 2000-126357/11.
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6169 GCTGCTCA 6162
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Philibert RA,
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This is the nucleotide sequence of a gene encoding a mouse SRY-related protein. The gene was isolated from a mouse genomic library using a cDNA fragment amplified by primers 133009-10 as a probe. The screen isolated 4 EcoRI fragments of 2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis revealed a 240 bp HMG box sequence between bases 7154-7393. Similarity with the human SRY HMG box sequence resulted in primers being generated to amplify the human SRY HMG box sequence for use as a probe to isolate the bovine SRY Telated gene (133008). The mouse and boyine genes are useful for determining the sex of an animal prior
                                                                                                                                         Bovine and mouse Sry-related DNA - useful for detecting e.g. the sex of unborn animals
                                        (KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU.
                                                                                                                                                                                                    Claim 1; Page 10-14; 21pp; Japanese.
94JP-0319525.
                                                                         WPI; 1996-336575/34
                                                                                                   P-PSDB; W03474.
30-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                               to birth
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ó 665 CTGCTCGTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACCACCACCA 724 Gaps ; 0 Ouery Match 2.7%; Score 35; DB 17; Length 10266; Best Local Similarity 53.2%; Pred. No. 2; Matches 74; Conservative 0; Mismatches 65; Indels 0

Sequence 10266 BP; 2958 A; 2202 C; 2228 G; 2878 T; 0 other;

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g ò

785 CTAACTCCCTTGGTGATGA 803 ò

Search completed: January 1, 2001, 03:47:19 Job time: 20447 sec

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     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                       Total number of hits satisfying chosen parameters:
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Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	DB ID	5 AA66	32 BE019	123	123 CNS04RW2	124 FR000694	124	7 AA940845	122	8 AI	121 CNS016	16 AV182303	124 FR0006	10 A1402	124 CNS05HX	121 CNSUU341	2 AA250	23	ထ	Ŋ	ഗ	œ 6	ک م	2 6	6 AA754683	36	39 R85066	10 AI43681	22 AWA4354	10 AT38816	34 B	121	123	11	50 AW02288	19 AV53012	97 AQ4580	123 CNS04C	35 BE40838	33 BE024	12 AI67017	13 AI87920
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ALIGNMENTS

RESULT AA664125

RESULT 2 BE019568/c

LOCUS	AA664125 ac06c04.s1 IMAGE:85565
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	clement;, AA664125, AA664125,1 EST. buman.,
REFERENCE	
AUTHORS	
TITLE JOURNAL COMMENT	".", "MOJE,", "STELLENDERSYN.", STEPTOE, M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project Unpublished (1997) Contact: Wilson RK
	Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
	Fig. 5.14 200 1010 Email: est@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES	Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 425. Location/Qualifiers
	/clone_lib="Stratagene lung (#937210)" /sex="male"
	/dev_stage="72 years" /lab_host="SoLR cells" (kanamycin resistant)" /note="Ordan: lung: Vector: pBluescript SK:: Site 1: EcoRI
	; Site_2: XhoI; Cloned unidirectionally, Primer: Oligo dT. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' -3'
BASE COUNT ORIGIN	51 a
Query Match Best Local Matches 12	watch 3.6%; Score 46.8; DB 5; Length 482; Local Similarity 48.8%; Pred. No. 0.0051; nes 126; Conservative 0; Mismatches 132; Indels 0; Gaps 0;
0v 727	38C
	CTGCTGCTGCTGCTGCTGTTGTTGTTTGTTTGTTGTTGCAGCTGCAGCTTGTTTGCTT 272
Qy 787	AACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCC 846
Db 273	CTGCTGTATCTGTTGCT
Oy 847	AACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACT 906
Qy 907 Db 393	CCTATGGAGATGGGTCTTCGTGTTGCTGGGTTCGCTGGTCTCACTGCTGCT 966
Qy 967	CCTAACTGGAAGCGTGCT 984
Db 453	GCTGTAGCGCCGCCTGCT 470

Tue Jan

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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | In the continuation of california, berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Image.linl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
                                                                                                                                                                              Euteleostomi;
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BE019568 526 bp mRNA EST 06-JUN-2000 ba031f05, yl NIH MGC_21 Homo sapiens CDNA clone IMAGE:2907009 5' similar to TR:015413 015413 CTG7A ; mRNA sequence. BE019568.1 GI:8279646
                                                                                                                                                                                                                    1 (bases 1 to 526)
NIH MGC http://www.ncbl.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 0.024;
0; Mismatches 124; Indels 0
                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                     Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                        Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.4%;
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                                                                                                                                                     ORGANISM
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AUTHORS
TITLE
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracodon.

Location/Qualifiers
1.970
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                                                                                                                                           GSS: genome survey sequence.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Tetracodon nigroviridis

Buxayota: Metazoa: Chordata; Craniata; Vertebrata; Eutcleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Buxypterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Buxypterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Tetracodoutiformes; Tetracodoutoldei; Tetracodoutidae; Tetracodon.

1 (bases 1 to 970)

1 (bases 1 to 970)

Neost-Crollius, H., Jaillon, O., Dasllva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J., and
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
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970 bp DNA GSS 17-MAY-2000 nigroviridis genome survey sequence T7 end of clone library G from Tetraodon nigroviridis, genomic survey
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2; Mismatches 176; Indels
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/db_xref="taxon:99883"
/clone="026011"
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883 GCTTCTGGAAAGTTCATCGCTACTCCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTT 942
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                       Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 005C20 of library H from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                 Neoteleostei;
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Unpublished
                                                                                                                                                                                                                                                                                          Golfacanthopterygii; Acanthopterygii; Percomorpha; Bolfacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontliformes; Tetraodontoidei; Tetraodontlidae; Tetraodon. 1 (bases 1 to 805)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C. Weissenbach, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Roest-Carollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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Pred. No. 0.031;
0; Mismatches 186; Indels
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/db_xref="taxon:99883"
/clone="005c20"
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/note="Genoscope sequence ID
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 GTTGTTGCTGCTGCTGTTGTTGCT 391
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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AL304427.1 GI:8192034
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Best Local Similarity 45.6%;
Matches 156; Conservative (
                                                                                     805 bp
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FR0006944 619 bp DNA GSS 02-MAR-1997
F.rubripes GSS sequence, clone 133B16aC7, genomic survey sequence.
867
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                                  943 GAGTTCGCTGGTCTCACTGCTCCTAACTGGAAGCGTGCT 984
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Pred. No. 0.099;
0; Mismatches 176;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_11b="cosmid 133B16"
/clone="133B16ac7"
150 c 116 q 175 t
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Conservative
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequenching project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Burypterygii; Neopterygii; Acanthomorpha; Burypterygii; Ctenosquamata; Acanthomorpha; Burypterygii; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon. 1 (bases I to 1003)
Rosst-Crollius; H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished

2 (bases 1 to 1003)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using
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752 bp mRNA EST 25-NOV-1998
LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD23113 5prime similar to M32221: fs(1)h
FBgn0004656 PID:9157453 SWISS-PROT:P13709, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             726 ACCAACAGTAGGGAGCATGCTGCTGCAGCTGCTGCTGCTGCTGTAGCTGCTGCTGCTGCT 785
                                                                                                                                                                                                                                                Charaterization and repeat analysis of the compact genome of freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          772 TCCAAGTCTCTTGCTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATAC
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Pred. No. 0.52;
0; Mismatches 136; Indels
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Best Local Similarity 47.3%;
Matches 122; Conservative
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3 (bases 1 to 1003)
Genoscope.
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                                                                clone 133B16dB11, genomic survey sequence.
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                                       18-SEP-1997
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/db_xref="taxon:31033"
/clone_lib="cosmid 133B16"
/clone="133B16dB11"
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GSS: genome survey sequence.
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Tetraodon nigroviridis
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Matches 139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                           Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostel; Neoteleostel;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygli; Neopterygli; Teleostei; Euteleostei; Neoteleostei Eurypterygli; Ctenosquamata; Acanthomorpha; Buacanthomorpha; Holacanthopterygli; Percomorpha; Tetraodontiformes; Tetraodontoidel; Tetraodontidae; Tetraodon. (bases 1 to 906)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetraodon nigroviridis genome survey sequence T7 end of clone 141P2. Of library G from Tetraodon nigroviridis, genomic survey sequence
                                                                                                                                                                   Contact: Harvey, D.

G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGCTAACGGTGGAGAGTTCGTGTCTGCTGTTATCGGATTCGAGACTGAAGGTCGTG 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701 CTCTCAAGGGTATCACCACCACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAG 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 761 CTGGTGCACACTCCAAGTCTCTTGCTAACTCCCTTGGTGATGACATCCCATTGGATAC 818
                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_atge="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGTGCGTCTGCTGCTGCTGCTGTTGTTGCTGCTGCATTGCATCTGCTGC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 3.1%; Score 40; DB 7; Length 752; Similarity 51.1%; Pred. No. 0.62; 91; Conservative 0; Mismatches 87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87; Indels
                                                                                                                                                                                                                                                                                  Plate: 231 row: B column: 1
High quality sequence stop: 639.
Location/Qualifiers
1. 752
/organism="Drosophila melanogaster"
/db_rsef="taxon:7227"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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ORIGIN
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JOURNAL
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VERSION
KEYWORDS
SOURCE
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AUTHORS
                                                                         REFERENCE
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                                                                                                                                                                       COMMENT
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon higroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

1. .906
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2 (bases 1 to 906)

Roest-Crollius, H., Jalllon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F.,

Saurin, W. and Weissenbach, J.

Human gene number estimate provided by genome wide analysis using

Tetroodon nigroviridis DNA sequence
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Expressed sequence characterization during appressorium formation in rice blast fungus, Magnaporthe grisea
Unpublished (1998)
Contact: Dean, R.A.
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 5737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI069309 946 bp mRNA EST 09-DEC-1999 mgae0006cC09f Magnaporthe grisea Appressorium Stage cDNA Library Pyricularia grisea cDNA clone mgae0006cC09f 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : COAG141DC11LP1~end : T7"
5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 717 CACCACCAACGGTGTTCTTGCTGTTGATCCAGCTGTTGTTGCAGCTGGTGCACACTCCAA 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               777 GTCTCTTGCTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACAT 836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  598 CACCAACAGTAGGGAGCATGCTGCTGCTGCTGCTGCTGCAGCWGCTGCTGCTGCTGC 657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="14F122"
/clone="lb="G"
/note="Genoscope sequence ID : COAC
a 271 c 259 g 216 t 5
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Best Local Similarity 47.2%;
Matches 118; Conservative
                                                                                                                                                                                                       (bases 1 to 906)
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Pyricularia grisea
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                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                     Genoscope.
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Alain Bucheton

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Gaps

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601 778 661 781

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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioldea
Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Koharary. Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H.,
Nishigaki,A., Motchashi,T., Zeng,O., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Ilda,K., Uesugi,H., Sugiyama,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV182303 300 bp mRNA EST 21-JUL-1999 AV182303 Yuji Kohara unpublished CDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans CDNA clone yk635h6 3', mRNA sequence. AV182303. GI:5562204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  557 TSTCBTKTYBTTTTSTGTTKKSGTGTKGKGTKGKRGKTGKRTKSKVKGTGGSTKBTYH 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 ACCTIACCGTGTACCGTGGAGAAGCAGACTTCGCCAGGGACCGTGGAGGTTGGGAACTTC 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 CTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGTC 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         482 GTCGTCTCAACGGTGTTCGTACTCAAATCCTCAGCGCTGATGCATTGCGTGATTTCGATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             662 TGTCTGCTCGTGTTATCGGATTCGAGGCTGAAGGTCGTGCTCTCCAAGGGTATCACCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           722 CCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACTCCAAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 CTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAAACGGTCACCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1101;
project grant. The DNA was prepared from embryos by and Genevieve Payan. It has been constructed in the
                                                                                                                                                                                                                                                                                                             others
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1 Similarity 22.0%; Pred. No. 1.1;
94; Conservative 134; Mismatches 199; Indels
                                                                                                                1. .1101
/organism="Drosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16L20"
                                                                                                                                                                                                                                                                                                          ب
                                                                                                                                                                                                                                                                                                          226
                                                                        Location/Qualifiers
1. .1101
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71 c 171 g
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Contact: Yuji Kohara
Gene Library Lab
                                                      pBeloBAC11
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AUTHORS
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a Collaboration of this BAC-end sequence was carried out as part of a Determination of this BaC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a Dettro-indeproper of this BAC-end sequence was carried out as part of a Dettro-indeproper of this BAC-end sequence was carried out as part of a Dettro-indeproper of this BAC-end sequence was carried out as part of a Dettro-indeproper of this BAC-end sequence o
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACN16L2O of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                  1. .946
//organism="Pyricularia grisea"
/strain="70-15"
/db_xref="taxon:89476"
/clone="mgae0006cC09f"
/clone="lib="Magnaporthe grisea Appressorium Stage CDNA
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                 Email: rdean@clemson.edu
Seg primer: T3 primer (AATTAACCCTCACTAAAGGG)
High quality sequence stop: 403
Location/Qualifiers
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Best Local Similarity 47.7%;
Matches 116; Conservative C
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Matches 132; Conservative
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(bases I to 567)

Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrania, Y., Milliams, G. and Brenner, S.

Direct Submission

Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CBIO 1SB. Email: blohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0006951 567 bp DNA GSS 02-MAR-1997 cubripes GSS sequence, clone 133B16bB5, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 AGGTCATGGCGCCTTTTGGAATGTTAACTGGTGGTGGTGGTGGGCGGGTCTGATCA 165
                                                                                                                                                                                                                                                                                                                                                                             658
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                                                                                                                  /organism="Caenorhabditis elegans"
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohra@lab.nig.ac.jp.
Location/Qualifiers
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/db_xref="taxon:31033"
/clone_lib="cosmid 133B16"
/clone="133B16bB5"
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                                                                                                                                                                                                                                                103
                                                                                                                             /strain="N2"
/db_xref="taxon:6239"
/clone="yk635h6"
/clone=lb="Yujl Kohara u
hermaphrodite embryo"
/sex="hermaphrodite"
                                                                                                                                                                                                                               /dev_stage="embryo"
59 c 86 g
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Fugu rubripes.
Fugu rubripes
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Best Local Similarity 48.6
Matches 105; Conservative
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                                                                                                                         201 TGCTGCTGCTACTGCTGCTACTGCTGCTGCTGCTACTGTTGCTGCTGCTGCTGC 260
                                                                                                                                                                                                                                                                                                                                                                                                              261 TGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACTGCTGCTGCTGCTGCTAC 320
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Furryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Ditera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilae; Drosophila.

1 (bases 1 to 612)
Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokst, P., Lewis, S. and Rubin, G.M.

BDGP/HHMI Drosophila EST Project
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 221 row: G column: 5
High quality sequence stop: 573.
Location/Qualiflers
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51.1%; Pred. No. 1.3;
iive 0; Mismatches 87;
                                               0; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Score 39;
Pred. No. 1
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AI402856.1 GI:4245943
  3.0%;
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Tue Jan

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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii: Neopterygii: Teleostei; Euteleostei; Neoteleostei;
Eurypterygii: Ctenosquamata; Acanthomorpha: Euacanthomorpha;
Holacanthopterygii: Acanthopterygii: Percomorpha;
Tetraodontiformes: Tetraodontoidei; Tetraodontidae; Tetraodon.
1 (bases 1 to 1076)
1 (bases 1 to 1076)
Bouneau.L., Baillault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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cost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                     CNSO5HXN 1076 bp DNA GSS 26-MAY-2000
Tetraodon nigroviridis genome survey sequence T3 end of clone
014F03 of library A from Tetraodon nigroviridis, genomic survey
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/clone_lib="A"
/note="Genoscope sequence ID : C0AA014CC02A1-end : T3"
1 260 c 309 g 333 t 14 others
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	Description	AR016592 Sequence	115325 Sequence 4	I15324 Sequence 3	AR016591 Sequence	AR016593 Sequence	I15326 Sequence 6	AR016594 Sequence	T15327 Sequence 7	AR016595 Sequence	I15328 Sequence 8	AR016604 Sequence	115337 Sequence 17
SUMMARIES	ID	AR016592	115325	115324	AR016591	AR016593	115326	AR016594	115327	AR016595	I15328	AR016604	115337
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                   TCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTACAACCACG
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Barry, G.F. and Kishore, G.M.
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Patent: US 5463175-A 3 31-0
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 4 31-OCT-1995;
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120 ATCHCTCARARCARCARCARARASCTARCCARCCARACCCCARACCCCCARACCCCCCCARACCCARACCACACACACACACACACACACACACACACACACACACA	61 GCGCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTCAACCCGAACCCTGGC 12 100 CCCTGATGCTTCAGCGCCGCGGATTCAAAGTCACCTTGATTCAACCCGAACCCTGGC 12 100 CCCTGATGATGATGATGATGATGATGATGATGATGATGATGAT	121 GAAGGTGCATCGTTTGGAATGCGGAATCACTTGATTGACCCGAACCCTCTGGC Z 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCGTCGTCGTCGTCCTTTGTTTTTTTT	240 181 300	241 TCCGGTTCAGCTATTTCCAACCATCATGCCTGGTTCATTCGCTTTCTGTTAGCCGGAAGA 3	301 CCAAACAAGGTGAAGCAGGGGAAAGCACTCCGCAATCTCATCAAGTCCAGGGGGCCT 360 111111111111111111111111111111111	/ 361 CTGATCAAGTCATTGGCGGAGGAGGTGATGCGAGCCATCTGATCCGCCATGAAGGTCAT 420	421 CTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTGCGG 480 	4 81 CGTCTCAACGGTGTTCGCACGCAGATCCTCAGCGCCGATGCGTTGCGGATTTCGATCCG 540	/ 541 AACTTGTGGCATGGGTTTACCAAGGCATTCTTATAGAAGGACGGTCACACGATTAAT 600	601 CCGCAAGGCCTCGTGACCCTCTTGTTTCGCCGTTTTATCGCGAACGGTGGCGAATTCGTA 660 11111111111111111111111111111111111	/ 661 TCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAGGCATTACAACCACG 720 	721 AACGGCGTTCTGGCCGTTGATGCAGGGTTGTCGCAGCCGCGCACTCGAAATCACTT 780 	781 GCTAATTCGCTAGGCGATGACATCCGGCTCGATACCGAACGTGGATATCATATCGTCATC 840	941 GCGAATCCGGAAGCCGCTCCACGCATTCCGACGGACGGTGCGTCAGGAAATTCATCGCG 900	901 ACACCTATGGAAATGGGGCTTCGCGTGGCGGTACGGTTGGGTTCGCTGGGCTCACAGCC 960	961 GCTCCTAACTGGAAACGTGCGCATGTGCTCTATACGCACGC	1021 CTCGCGCCTGCGAGTTCTGAAGAACGATATTCCAAATGGATGG	7 1081 CCGGATTCGCTCCCCGTGATTGGCCGGGCAACCCGGACGTAATCTATGCTTTC 1140
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Barry,G.Francis and Kishore,G.Murthy.
Glyphosate tolerant plants
Patent: US 57/6760-A 3 07-JUL-1998;
Location/Qualiflers
1. 1692 Ļ GGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1293 Similarity 99.8%; Score 1260; C Similarity 99.8%; Pred. No. 0; 13; Conservative 0; Mismatches 361 5776760 /organism="unknown" 1 480 c 469 g AR016591 1692 bp DNA Sequence 3 from patent US 5: AR016591 GI:3972868 9 Unknown. Unclassified. ø . Unknown. 381 1.293;

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BASE COUNT 286 a 368 c 361 g 281 t	atch 97.1%; Score 1255.2; DB 5; Length 1296;	Matches 1290; Conservative U; Mismatches 3; Indels 3; Gap 1 ATGTCTGAGAACCACAAAAAGTAGGCATCGCTGGACCGGAATCGTCGCGTATGCACG 6 1 ATGTCTCAGAACACACAAAAAGTAGGCATCGCTGGACCGGAATCGTCTATTTTTTTT	DD 1 AFGGCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTGGCGGTATGCACG 60 Qy 61 GCGCTGATGCTTCAGCGCGGGATTCAAAGTCACCTTGATGACCCGAACCCTCGGC 120 Db 61 GCGCTGATGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	121 GAAGGTCCATCGTTGGGAATGCCGGATGCTTCAACGCTCATCGTCGTCCTATGTCC 1 121 GAAGGTCCATCGTTTGGAATGCCGGATGCTTCAACGCTCATTCGTCGTCGTCCTATGTCC 1 121 GAAGGTCCATCGTTCAATGCTTCAACGCTCATCGTCGTCGTTCGT	181 AFGCCGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCGAT-GGCCGTTGTCA 2	240 ATCCGGTTCAGCTA-TTTCCAACCATCATCATCATCATTCATTAGCTTCTTAAGCTTAGCTTAAGCTTAAGCTAACCATCATGCATCATTAAGCTAATTCGCTTTAAGCTAACCATCATGAACCATCATGAATCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAATTCAAACCATAAACCAATAAACCAATAAACCAATAAACCAATAAACCAATAAACCAATAAAACAAAAAA	298 AGACCAAACAAGGGAAGGAGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 301 AGACCAAACAAGGGAAGCAACCCCCGAAAGCAATCCTATCAACAAGTCCAGGGTG 301 AGACCAAAGTCAAGAAGCAGGGGAAAACCACTCCGCAAATCTCATCAACAAGTCCAGGGGG	3T 4 T 1 5	418 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTG 47 421 CATCTGACCGTATATCGTGGAAAGCAGAACTTTGCCAAGGACGAGGAGAACTG 48	478 CGCCGTCTCAACGGTGTTCCCACACTCCTCAGCGCCGATGCGTTCGCGGATTTCGAT 53 481 CGCCGTCTCAACGGATGTCCCACACTCTCACCGCCGATGCTTCGAT 54 CGCCGTCTCAACGGTGTTCGCACGCAACCTCACCGATGCCGATGCGGATTTCGAT 54	CCGAACTIGTCGCATGCCTTTACCAAGGCCATTCTTATAGAAGACAGGTCACAGGATT 59 	598 AATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCGTTTTATCGCGAACGGTGGCGAATTC 601 AATCCGCAAGGGCTCGTCTCTTTTTTTTATCGCAACGGTGGCGCAATTT 6	GTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGGCGCGCTTAAAGGCATTACAACC 71	0y 718 ACGAACGCGTTCTGGCCGTTGATGCAGCGGTTGTCGCAGCCGGCGCACACTCGAAATCA 777	Qy 778 CTTGCTAATTCGCTAGGGGATGACATCCGGATACCGAAGGTGGATATCATATCGTC 837	Qy 838 ATGGGAATCCGGAAGCCGCTCCACGCATTCCGACGATGCGTCAGGAAAATTCATC 897	898 GCGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTCGCTGGGCTCACA 9	Db 901 GCGACACCTATGGAAATGGGGCTTCGCGTGGGGGTTGAGTTCGCTGGGGCTCACA 960 Qy 958 GCGGCTCCTAACTGGAAACGTGGGATGTGCTCTATACGCACGC
Db 600 CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCAGCGCCGATGCGTTGCGGATTTCGAT 659	Oy 538 CCGAACTTGTCGCATGCGTTTACCAAGGCCATTCTTATAGAAGAGAACGGTCACACGATT 597	Oy 598 AATCCGCAAGGCTCGTCACCCTCTTGTTTCGCGGATTTTATCGCGAACGGTGCGAATTC 657	Oy 658 GTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGCGCTTAAAGGCATTACAACC 717 111111111111111111111111111111111	718	Oy 778 CITGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC 837	QY 838 ATCGCGAATCCGGAAGCCGCTCCACGATTCCGACCATGCGTCAGGAAATTCATC 897	898 GCGACACCTATGGAAATGGGGCTTCGCGGGGGGTACGGTTGACTTCGCTGGGCTCACA 9 111111111111111111111111111111111111	Oy 958 GCCGCTCCTAACTGGAAACGTGCCCATGTGCTCTATACGCACGC	<pre>Qy 1018 GCCTCGCGCCTGCGAGTTCTGAAGAACGATATTCCAAATGGATGG</pre>	1078 ATCCGGATTCGCTCCCGTATTGGCCGGCAACCCGGACACCCGACGTAATCT 11	OY 1138 TTCGGCCATGGTCATCTCGGCATGACGGGCGCCGATGACCGCAACGCTCGTCAGAG 1197	e c	Oy 1258 ATTGGCAAATCCAAGCGGTCCGGCAAGTTAA 1293 	AR016593 1296 bp DNA	GI:3972870	_	8 G 8	

QY 358 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCAACCGCATGAAGGT 417	18 ACGAACGCGTTCTGGCCGTTGATGCAGCGGTTGTCGCAGCCGCGCACACTCGAAATCA	09 GCGCTCCTAACTGGGAATGGGCCTTCGCGGGTACGGTTCACTGGGCTCACA 960 09 958 GCCGTCCTAACTGGAAACGTGCGCATGTTCCTATACGCACGC		RESULT 7 AR016594 LOCUS AR016594 LOCUS LOCUS DEFINITION Sequence 7 from patent US 5776760. ACCESSION AR016594 VERSION AR016594.1 GI:3972871 KEYWORDS SOURCE UNKNOWN.
	TESULT 6 TESULT 7 TESULT 7	### Second 1.1286	0.0 0.1 0.0 0.1	OY 240 ATCCGGTTCAGCTA-TTTCCAACCATCATG-CCTGGTTGATTCGCTTTCTGTTAGCCGGA 297

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Pred. No. 0;
0; Mismatches
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Barry, G.F. and Kishore, G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 7 31-OCT-1995;
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US 5463175.
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Pred. No. 0;
0; Mismatches
                1 (bases 1 to 1296)
Barry, G. Francis and Kishore, G. Murthy
Glyphosate tolerant plants
Patent: US 5776/60-A 7 07-JUL-1998;
Location/Qualifiers
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                                                                     /organism="unknown"
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Best Local Similarity 95.0%;
Matches 1231; Conservative
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Unknown.
Unclassified
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240 ATCCGGTTCAGCTA-TTTCCAACCATCATG-CCTGGTTGATTCGCTTTCTGTTAGCCGGA 297 [111111111111111111111111111111111111		GTATCTGCGCGTGTTTTTGTTTTTTTTTTTTTTTTTTTT		ATCCGGATTGCTCCCGTGATTGCCGGCCACCCGACGCGACGCGACTATGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTTGCTTGCTTTGCTTTGCTTTGCTTGCTTTGCTTGCTTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGCTTGTTG
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Pred. No. 3e-244;
O; Mismatches 207;
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y.G. Francis and Kishore, G.Murthy.
hosate tolerant plants
nt. 18 5776760-A 8 07-JUL-1998;
Location/Qualiflers
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8 from patent US 5776760.
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                 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCGCTATGTCC
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                                         CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC
                                                                            ATCCCCAATCCCCAAGCCCCTCCACCCATTCCCACCCATCCGATCCGTCAGGAAATTCATC
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Barry, G.F. and Klshore, G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 8 31-OCT-1995;
Location/Qualifiers
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llarity 83.8%;
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Db 541 CCTAACTTGTCTCACGCC Qy 598 AATCCGCAAGGCTCGTC	718 721 778 778 838 841 841 958	Oy 1018 GCCTCGGGCCTGGGAGT Db 1021 GCTCTGGCCTGCCAGT QY 1078 ATCCGGATTGCTTCTC QY 1078 ATCCGGATTGCTTCCT QY 1138 TTCGGCATGCTTCCTTCCA QY 1138 TTCGGCATGCTTCCTTCCTTCC QY 1138 TTCGGCATGCTTCCTTCCTTCCTTCCTTCTTCTTCTTCTTCTTCTTC	RESULT 12 115337 115337 115337 115337 129 DEFINITION Sequence 17 from ACCESSION 115337.1 GI:125 KEYWORDS 115337.1 GI:125 SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. Unclassified. AUTHORS BAITY, G.F. and K TITLE Glyphosate toler JOURNAL Patent: US 54631 FEATURES SOURCE JOCATIO AUTHORS 1. 129 SOURCE JOCATIO ONEGIN QUETY MATCH 71
Oy 1198 CTCCTCGCAGGCGAAAAGACCTCAATCGACATTCGCCCTTCGCACCAAACCGCTTTGGT 1257	RESULT 11	Ouery Matches Matches 1 1 61 121 121 181	0y 240 ATCCGTTCAGCTA-TTTCCAACCATCATGCC-TGGTTGATTCGTTTGTTAGCCGGA 297 1

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ed. No. 2.3e-243;
Mismatches 209;
Pred.
Similarity 83.6%;
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Best Local Sim
Matches 1084;
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4 Arabidopsis sp.
Arabidopsis sp.
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Rosidae; Capparales; Brassicaceae; Arabidopsis. GCTCTCGCTCCTGCCAGTTCTGAAGACGTTACTCCAAGTGGATGGGTTTCCGTCCAAGC 1080 1201 CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAAACCGTTTCGGT 1260 180 453 218 513 272 332 633 333 393 9 06-MAR-1998 Gaps 1 ATG/TCTGAGAACCACAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC TTCGCCCATGGTCATCTCGCCATGACAGGGGCGCCGGATGACCGCAACGCTCGTCAGAG CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGT ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCT--------GTTGATTCGCTTTCTGTTAGCCGGAAGACCAAACAAGGTGAAGGAGCAGGCGAAAACACT GTTGATTCGTTTCTTGCTTGCTGGAAGACCAAACAAGGTGAAGGAGCAAGCTAAGGCACT ATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAACCCGGACGACGTAATCTATGCT 53; Length 1631; Indels PAT 66.3%; Score 857.6; DB 5; 80.2%; Pred. No. 1.1e-224; ive 0; Mismatches 214; ب INDUCIBLE HERBICIDE RESISTANCE Patent: WO 9706269-A 1 20-FEB-1997; ZENECA LTD (GB) 454 WO9706269 /organism="Arabidopsis /db_xref="taxon:29726" 454 c 381 g 4 Location/Qualifiers 1631 bp rom Patent (A59869.1 GI:3715060 (bases 1 to 1631) .1631 Best Local Similarity 80.2 Matches 1079; Conservative

1 (bases 1 to 3430) Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C. Nucleotide sequences of hydroxyproline specific alpha-ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas

Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group; Pseudomonas.

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ACACALAWAAFDGYRETTLEGRAQFLETTAYOLEALGDALIDRAVESGLPKARIQGE
AQACALAWAAFDGYRETTLEGRAQFLETTAYOLEALGDALIDRAVAESGLPKARIQGE
REGTCTQLIPRORVARAGEMLDYRVDAAOPERODLPRADLEGRAVEGANAFEGSANF
PURFSYNGGDTAAAGCPVYKARISAHPGTSELVGQANAQANKLGGLPAAVFESLN
GSGREVGIALVSDPRIKAVGFTGSRSGGIALCOATQARPEPIPVYABMSSINPVFLFE
AALQARAEALANGFYAGTGSRSGGTALCOATQARPEPIPVYABMSSINPVFLFE
MLTPGIFSSANGANAVQAAASGQAQGCQFNOCQAQLFVTQABAFLADPALQA
EVFGAASLVVACASBECHQVARAHLEGQLTATLQLDDADIDRARALLFTLERKAGRIL
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/transl_table=11 /product="ketoglutarate semialdehyde dehydrogenase" /protein_id="AAAA25698.1" /db_xref="G1:150982"

/gene="ketoglutarate semialdehyde dehydrogenase" /gene="ketoglutarate semialdehyde dehydrogenase"

۲. 2626 2567 CGGGCACCTGGCCACCGAGCAGGTGTTCCCGATTGCCGACCTGTCGATCCTCAAGCGCT 2387 GGCCATGCCTGGTTCACCCGCCTGCTCAACCTGCGCCCGGCCCCGTTCCAGCGCA 2507 202 259 379 CGCCGTGGTGGCCCCCGGGATTGTCGCCTTGCCTGTGCCTTGCAACTGGCCCGCCAGG 2267 CCATCATGCCTGGTTGATTCGCTTTCTGTTAGCCGGAAGACCAAACAAGGTGAAGGAGC 319 439 ATTCAAAGTCACCTTGATTGACCCGAACCCTCCTGGCGAAGGTGCATCGTTTGGGAATG 142 Gaps 82 AGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACGGCGCTGATGCTTCAGCGCCGCG TGTGGCCGGCATCCGCACGCTGAACGAAGGCAGCCTGGGTGCATGGCAGCGCCTGCTGG CGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCCATGCCGGGAAACTTGACGAGCG GCCGAAGTGGCTCCTTGACCCGATGGGC---CGTTGTCAATCCGGTTCAGCTATTTCCA GGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGCGG AGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCGTGGAG 6.5%; Score 84.2; DB 2; Length 3430; 46.2%; Pred. No. 2.7e-12; iive 0; Mismatches 608; Indels 18; 537; Conservative Similarity qq à

440 AAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTGC-GGCGTCTCAACGGTGTTCGC 498

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PSEAKSD 3430 bp DNA BCT 26-APR-1993 Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase gene, complete cds.

PSEAKSD LOCUS DEFINITION RESULT 14

us-08-484-274-4.rge

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Query Match
Best Local 3
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Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
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Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
gene, complete cds.
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2627 CCTGAGTCACGCCACGCACTGGAGCGTTGCCACCCCATGCAACAGCAGCGGGTGCCG 2686
                                                                                                                                                                                                                                  2807 GAACTGTTCGAAGCGGCCAAGGCCAGCGGCGTGCGCTTTGTTCAGGCGCAGGTCGATGGC 2866
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                                                                              GTGGACGTCTGGTCGCCGAAACCGTGCGCGGAGCCAACTGAACTGAGCCCGTCACTG
                                                                                                                                                                                                                                                                                                                                                                              2927 CAGGTGCTGATCAGCTGTGGTGCCCATTCTGCGAAACTGACCGCCGCGCGTGACGGGCAAG
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                                                                                                                                                            2747 CIGGGCGGGTTGTTCTTTCCGCGCACCTCGTCGACCCTTACCGGGTTGTGTGC
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                                                   ACGCAGATCCTCAGCGCCGATGCGTTGCGGGATTTCGATCCGAACTTGTCGCATGCGTTT
                                                                                                                          ACCAAGGGCATTCTTATAGAAGAGAAGGGTCACACGATTAATCCGCAAGGGCTCGTGACC
                                                                                                                                                                                                619 CTCTTGTTTCGCCGTTTTATCGCGAACGGTGGCGAATTCGTATCTGCGCGTGTCATCGC
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Pseudomonas putida (strain ATCC 12633) DNA.
Pseudomonas putida
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/organism="Pseudomonas putida"
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EDACALAWARPDRY RETSLATRAEFLETIAAEIEALGBELLDRAVAETGLPRARILGE
RGRCALAWARPDRY RETSLATRAEFLETIAAEIEALGBELLDRAVAETGLPRARILGE
RGRTGOOLRTFARTVERGEWLDVRVDAALPERGPLPRADLRORGIALGPVAVFGASNF
PLAFSYNGGDTASALAAGCYVKARIBAHPGTSELVGRAVRRAVORSALPEGVFSLLF
GSGREVGIALVSDPRIKAVGFTGSRSGGMALINAAQARLEPIPVYAEMSSINPVLLFP
MALEARGEAALOGFVASLTOGGGGCFTORFGLVARRGGPALDAPRIRAAANLVORSPAOT
MLTPGIFSAYENGVFTLAEWITHAGOLTATLHLDDADLESARALLPVLERRAGRILV
GNGPTGVREVCDANVHGGPFPATSDAFTTSVGTAAILRFLRPVCYQDFPDTLLPAALQH
GNGPTGVREVCDANVHGGPFPATSDAFTTSVGTAAILRFLRPVCYQDFPDTLLPAALQH
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                                                                                                                                                                                                                        /product="Ketoglutarate semialdehyde dehydrogenase"
/protein_id="AAA25870.1"
/db_xref="GI:151318"
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                                                                                                                         /gene="ketoglutarate semialdehyde dehydrogenase"
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/note= _glyphosate oxidoreductase coding
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                                                                                                                                                                             1 ATGTCTGAGAACCACAAAAA......AAACGGGTCCGGCAAGTTAA 1293
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                   480022 seqs, 187831343 residues
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Listing first 45 summaries
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                                         ccgcaagggctcgtgaccctcttgtttcggcgttttatcgcgaacggtggcgaattcgta
                                                                   TCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGCGCGCTTAAAGGCATTACAACCACG
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/note= "glyphosate oxidoreductase coding region"
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/note= "not page 1/377.
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                                                                                                                                                                                                 The sequence is that of a gene encoding a glyphosate oxidoreductase (GOR) enzyme. It was obtd. from bacterial isolate LBAA. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields conty. crops. This sequence (SEQ ID No.3 in the specification) contains apparent discrepancies (see feature table) with a supposedly identical sequence (fig 2), since it is unclear from the specification which of these is correct, both sequences have been indexed. See also Q20833-Q20841 and Q22705 - the alternative
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                                                                                                                      Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate
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                                                                                                                                                                                                                                                                                                                                                               Sequence 1689 BP; 381 A; 477 C; 470 G; 360 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
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                                                                                                                                                                                                                                                                                                                                                                                                      99.8%; Score 1289.8; 99.8%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                         Claim 1; Page 93; 142pp; English.
 90US-0543236
                                                                                                                                                                                                                                                                                                                                    sequence for the GOR gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 1291; Conservative
                                                     Barry GF;
                           (MONS ) MONSANTO CO.
                                                                              WPI; 1992-041559/05
                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                            P-PSDB; R20642
 25-JUN-1990;
                                                     Kishore GM,
                                                                                                                                                 herbicide
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              CATCTGACCGTATATCCTGGAGAAGCAGACTTCGCCAAGGACCCGCGGAGGTTGGGAACTG
                                                                              AATCCGCAAGGCTCGTGACCCTCTTGTTTCGGCGTTTTTATCGCGAACGGTGGCGAATTC
                                                                                                                                                                                                                       GTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGGCGCCTTAAAAGGCATTACAACC
                                                                                                                                                                                                                                                                                                                             CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC
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                                                                CGGCGTCTCAACGGTGTTCGCACGCAGGATCCTCAGCGCCGGATGCGTTGCGGGATTTCGAT
                                                                                                                  CCGAACTTGTCGCATGCGTTTACCAAGGGCATTCTTATAGAAGAGAACGGTCACACGATT
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                                                                                                                                                                                                                                                                                         Manipulated glyphosate oxidoreductase gene
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                                                                                                                                                                                                                                                                                                                                               The sequence is that of a gene encoding a glyphosate oxidoreductase (GOR) enzyme. It was obtd. from bacterial isolate LBAA. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in flelds contg. crops. This sequence (fig 2) contains apparent discrepancies (see feature table) with a supposedly identical sequence (SEQ ID No.3 in the specification), since it is unclear from the specification which of these is correct, both sequences have been indexed. See also Q20833-Q20841 and Q20832 - the alternative sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATCCGGTTCAGCTA-TTTCCAACCATCATG-CCTGGTTGATTCGCTTTCTGTTAGCCGGA
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 alternative sequence"
                                       alternative sequence'
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Pred. No. 0;
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"not present in
 present in
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/note= "not
392.
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900S-0543236.
                                                                                                               91WO-US04514
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                         /*tag-
/note-
                                                                                                                                                                                                         Kishore GM, Barry GF;
                                                                                                                                                                                (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                 WPI; 1992-041559/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the GOR gene
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          misc_feature
                                                                                                              24-JUN-1991;
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25-JUN-1990;
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                        Location/Qualifiers
9..1304
/*tag= a
/note= "encodes wild type glyphosate oxidoreductase"
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                                                                                                                                                                                                                                                                                                                                                                                             13; Length 1321;
                                                                                                                                                                                                                     Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate
                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                   T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                                                                                                                                            Score 1253.6;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1321 BP; 292 A; 373 C; 369 G; 287
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                                                                                                                          91US-0717370
90US-0543236
                                                                                                         91WO-US04514
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Best Local Similarity 99.5
Matches 1289; Conservative
        isolate LBAA
                                                                                                                                                                         GF;
                                                                                                                                                      (MONS ) MONSANTO CO
                                                                                                                                                                                          WPI; 1992-041559/05
                                                                                                                                                                        GM, Barry
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                                                                                                         24-JUN-1991;
                                                                                                                          24-JUN-1991;
25-JUN-1990;
                                                                                        09-JAN-1992
        Bacterial
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CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGGGGGTTGGGAACTG
                                                                                                                        CCGAACTTGTCGCATGCGTTTACCAAGGGCATTCTTATAGAAGAGAACGGTCACACGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGT
                                                             CGGCGTCTCAACGGTGTTCGCACGCAGGTCCTCAGCGCCCGATGCGTTTCGGATTTCGAT
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us-08-484-274-4.rng

368 417 428 477 488 537 548 597 608 657 999 717 728 777 788 837 848 897 908 957 896

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249 atccggttcagctatttccaaccatcatgccctggttgattcgctttctgttagccgga
                                                                                                    cctctgatcaagtcattggcggaggaggctgatgcgagccatctgatccgccatgaaggt
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                                      CGGCGTCTCAACGGTGTTCGCACGCAGGATCCTCAGCGCCGATGCGTTGCGGGATTTCGAT
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                          AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAG'TCCACGGTG
                                                                           CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCAAGGT
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It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant.

Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops.
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                                                                                    /note- "encodes wild type glyphosate oxidoreductase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFCCGGTTCAGCTA-TTTCCAACCATCATG-CCTGGTTGATTCGCTTTCTGTTAGCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1321;
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                                                                                                                                                                                                                                                                                                                    Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide
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                                               Location/Qualifiers
9.1304
/*tag= a
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94.98;
 Recombinant; GOR; resistance;
                                                                                                                                                                                        91US-0717370.
                                                                                                                                                                  91WO-US04514
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Matches 1230; Conservative
                         Bacterial isolate LBAA
                                                                                                                                                                                                                                                      Kishore GM, Barry GF;
                                                                                                                                                                                                                               (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                                                WPI; 1992-041559/05.
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                                                                                                                                                                24-JUN-1991;
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Transformed plants resistant to glyphosate can be obtd. so that the each can be selectively controlled in fields contg. crops.
                                                                                                                                                                                                                                                                                                                                                                                    Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1296 BP; 271 A; 359 C; 305 G; 361 T; 0 other;
                                                                         gene
                                                                      Synthetic glyphosate oxidoreductase
                                                                                                                                            Location/Qualifiers
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 BP
                                                                                             GOR; resistance;
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900S-0543236
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 DNA; 1296
                                               (first entry)
                                                                                                                                                                                                                                                                                                                            Barry GF;
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 standard;
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                                                                                               Recombinant;
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                                                                                                                                                                                                                                          24-JUN-1991;
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25-JUN-1990;
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                                                                                                         GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCCCTATGTCC
     Score 928.8; DB 13; Length 1296; Pred. No. 9.8e-288; ); Mismatches 207; Indels 3;
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      71.8%;
83.8%;
             Best Local Similarity 83.8
Matches 1086; Conservative
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                        AGACCAAACAAGGTGAAGGAGGAGGGGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capa of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
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                                                                                                                                                        Sugar beet, transformation; T-DNA; insertion; cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCCGGTTCAGCTA-TTTCCAACCATCATGCC-TGGTTGATTCGCTTTCTGTTAGCCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 928.8; DB 20; Length 84.18; Pred. No. 2.4e-287;
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M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.4e-287;
thes 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  plants
attggtaagtccaagcaaactggtcctgcatcctaa 1296
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                                                                                                                                                                                                                                                                                                                                                                                                 resistant transgenic sugar beet
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                                                                                                                                   Sugar beet T-DNA containing cp4/epsps #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 36-41; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                     Tenning
                                                                   BP
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83.8%;
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                                                                                                              (first entry)
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Matches 1086; Conservative
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                                                                 X57309 standard;
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                                                                                                                                                                                                     Beta vulgaris
                                                                                                             26-JUL-1999
                                                                                                                                                                                                                                                                      29-OCT-1998;
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A chemically inducible plant gene expression cassette which comprises an inducible promoter linked to a gene (I) that confers resistance to a herbicide, is calimed. (I) imparts resistance to N-phosphonomethyl.

Glycine (glyphosate) or its salts, but may also be a gene for resistance to, e.g. chlocoacetanilides, glufosinate, sulphonyl ureas, imidazolones, etc. The inducible promoter (e.g. alch, alck, alck, other alck induced gene promoter) is operatively linked to an alck regulator sequence.

Induced expression of (I) avoids the risk that constitutive expression of (I) avoids the risk that constitutive expression controlled by herbicide applied without inducer and minimises the chance that herbicide-resistant strains of weeds will arise. The expression cassette is strictly controlled and suitable for general use in plants (both mono- and dicctyledons). The alch/alck gene switch was exemplified with genes conferring resistance to glyphosate. The switch was used to citive inducible expression of glyphosate oxidace (COX) in plants.

Switchable GOX was expressed alone or in conjunction with constitutive expression of 5-enol-pytuvylshikimate 3-phosphate (EBSPS) CP4. Constructs were optimised for expression in mono- and dicctyledonous crop species. The present sequence comprises a fusion of the GOX gene fused to the chloroplast transit sequence if from Arabidopsis RUBISCO (CP71). This sequence was ligated into pwJB1 (see T8566) and used in construction of
                                                                                                                                                                 expression cassette; inducible promoter; alcA; alcA; regulator; alchol dehydrogenase; herbicide resistance gene; glyphosate; N-phosphonomethyl-glycine; glyphosate oxidase; GOX; EPSPS; 5-enol-pyruvylshikimate 3-phosphate CP4; chloroplast transit sequence 1; Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemically inducible cassette for expressing herbicide resistance gene in plants - and derived plants, partic. for resistance to glyphosate, avoids constitutive expression and minimises development of herbicide tolerant weeds
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  standard; DNA; 1631
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                              Chimeric Arabidopsis
                                                                                                                           CPT1-GOX gene fusion
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                                                                                                                                                                                                                                                                                                                     Synthetic.
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הכלתפנונים דרו יה אלה כי הרו מי אלה די ה סבוומדי

Ouery Match 66.3%; Score 857.6; DB 18; Length 1631;
Best Local Similarity 80.2%; Pred. No. 7.3e-265;
Matches 1079; Conservative 0; Mismatches 214; Indels 53; Gaps 4;
Oy 1 ATGTCTGAGAACCACAAAAAAGTAGGCATGGCGGGATTGCAGG 60

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1147 1113 1233 1027 332 692 742 907 967 633 392 693 452 753 632 933 993 787 1054 gigaaticaagcitacigcagitigitigcagciggigcacaciccaagtcitigciaact gaaggtgettettteggtaaegetggttgetteaaeggtteeteegttgtteeaatgtee GTTGATTCGCTTTCTGTTAGCCGGAAGACCAAACAAGGTGAAGGAGCAGCGGAAAGCACT 814 egetgatgeattgegtgatttegateetaacttgteteaegeetttaeeaagggaateet TTTTATCGCGAACGGTGGCGAATTCGTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGG 1114 cccttggtgatgacatcccattggataccgaacgtggataccacatcgtgatcgccaacc ACTGGAAACGTGCGCATGTGCTCTATACGCACGCTCGAAAACTTCTTCCAGCCCTCGCGC actggaagcgtgctcacgttctcacactcgtgctcgtaagttgcttccagctctcgctc 1088 CGCTCCCCGTGATTGGCCGGGCAACCCGGACGCGACGTAATCTATGCTTTCGGCCATG ----TGACCCGATGGGCCGTTGTCAATCCGGTTCAGCTA-TTTCCAACCATCATGCC-TG CCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGC CGCCGATGCGTTGCGGGATTTCGATCCGAACTTGTCGCATGCGTTTACCAAGGGCATTCT TATAGAAGAAAGGTCACACGATTAATCCGCAAGGGCTCGTGACCCTCTTGTTCGGCG TAGGGCGCTTAAAAGGCATTACAACCACGAACGGCGTTCTGGCCGTTGATG------788 GGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTCATCGCGAATC 848 CGGAAGCCGCTCCACGCATTCCGACGACCGATGCGTCAGGAAAATTCATCGCGACACCTA TGGAAATGGGGGCTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACAGCCGCTCCTA CTGCGAGTTCTGAAGAACGATATTCCAAATGGATGGGGTTCCGGCCGAGCATCCCGGATT ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCT-----1294 334 121 394 181 454 219 273 333 634 453 754 513 573 633 934 693 994 908 896 1028 1354 qq g qq q ò ò ò qq δ à ò pp à a δ a ò 9 ò a ò ò οp ò QQ qq g QQ Q ò ò ò ò ò

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Beta vulgaris
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                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGTCTGAGAACCACAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG 60
                                                                                                                                                                                                                                                                  Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
 cocttocagtgattggtcgtgctacccgtactccagacgttatctacgctttcggtcacg
                                 GTCATCTCGGCATGACAGGGGCGCCCGATGACCGCAACGCTCGTCTCAGAGCTCCTCGCAG
                                                             GCGNAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGTATTGGCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 8798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glyphosate resistant transgenic sugar beet plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.6%; Score 641.8; DB 20;
83.2%; Pred. No. 2.5e-195;
ative 0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                     (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                              Sugar beet T-DNA containing cp4/epsps
                                                                                                      CCAACCAAACGGGTCCGGCAAGTTAA 1293
                                                                                                                          1594 ccaagcaaactggtcctgcatcctaa 1619
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                                                                                                                                                                               X57308 standard; DNA; 8798
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Matches 766; Conservative
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herbicide;
                                                                                             CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGGGGGGTTGGGAACTG
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                                                                         ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGG - CCGTTGTCA
                                                                                                                                                240 ATCCGGTTCAGCTA-TTTCCAACCATCATGCC-TGGTTGATTCGCTTTCTGTTAGCCGGA
                                                                                                                                                                                                                          298 AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sugar beet T-DNA containing cp4/epsps fragment.
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                                                                                                                                                                                                                             CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC 837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"(sem1)aldehyde dehydrogenase-like protein"
complement (426949..428028)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation; legume; plant; ds.
                                                                                                                                                                                                                                                                                                   ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACGATGCGTCAGGAAAATTC 894
                                                           718 ACGAACGGCGTTCTGGCCGTTGATGCAGCGGTTGTCGCAGCCGGCGCACACTCGAAATCA
                                                                                                     GTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAAGGCATTACAACC
                                          /product= "aminotransferase-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "encapsulation-like protein"
/note= "homologous to the CapA gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "homologous to the OppF gene" 420774, 422159
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/note= "homologous to the OppD gene"
419677..420738
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424056..425594
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/note= "homologous to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
417796..418671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium species plasmid pNGR234a.
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V30458/c
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                                                                                                                                                                                                                                                                                                              descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7416 agaccaaacaaggtgaaggagcaagctaaggcactccgtaacctcatcaagtccactgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGG - CCGTTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 CCGAACTTGTCGCATGCGTTTACCAAGGGCATTCTTATAGAAGAAGAACGGTCACACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 ATCCGGTTCAGCTA-TTTCCAACCATCATGCC-TGGTTGATTCGCTTTCTGTTAGCCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT
                                                                                                                                                                                                                                                                                                   This invention describes a novel sugar beet plant, including its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 640.2; DB 20; Length 8012;
Pred. No. 7.9e-195;
0; Mismatches 138; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;
                                                                                                                                                                                                                                      Glyphosate resistant transgenic sugar beet plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49.5%; Score 640.2;
84.3%; Pred. No. 7.9
                                                                                                                                (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                                              PP;
                                                                                                                                                                                                                                                                     Claim 8; Page 24-29; 55pp; English.
                                                                                                                                                                               Tenning
                                                                      98WO-EP06859
                                                                                                  97US-0112003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 84.3
Matches 756; Conservative
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                                                                                                                                                                              Steen
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                                                                                                                                                                              Mannerloef M,
                                                                      29-OCT-1998;
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                                        14-MAY-1999
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/standard_name= "ORF L2"
/product= "gamma-hexachlorocyclohexane-dechlorInase-like
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454590.,456131
                                                                                                                                                                                                                                                                                                                                                                                                                         'gene= "nifk"
'product= "beta-subunit of FeMo protein of nitrogenase"
                                                                                                                                                                                                                                                    /product= "putative protein with degradative function" 450341..451396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name= "ORF L12"
/product= "protein similar to part of the Fe protein
                                                                                                                                                                                                                                                                                          /standard_name= "ORF L4"
/product= "luciferase alpha-subunit-like protein"
/note= "homologous to the LuxA gene"
452980..454494
                                                                     /product= "C4-dicarboxylate transport protein"
/note= "homologous to the DctAI gene"
446599..447843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF L8"
/product= "protein involved in FeMo co-factor
biosynthesis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product- "protein involved in FeMo co-factor biosynthesis"
                                                                                                                         /product= "cytochrome P450-like protein"
/note= "homologous to the CamC gene"
447844..448500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "ORF L10"
/product= "protein of unknown function"
/note= "homologous to the Nifx gene"
459579..460067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF L13"
/product= "protein of unknown function"
463201..464739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /standard_name= "ORF L11"
/product= "protein of unknown function"
                                                                                                                                                                                             protein" /note= "homologous to the LinA gene" 448497.,450203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "homologous to the NifB gene"
457687..459096
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461228..461545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "homologous to the FixF gene"
459093..459575
               /note= "homologous to the Nifo gene"
445088..446602
    /product- "ferrodoxin-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= aj
/standard_name= "ORF Ll4"
/product= "peptidase-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of nitrogenase"
                                                  /standard_name= "ORF K23"
                                                                                                                      /standard_name= "ORF L1"
                                                                                                                                                                                                                                                /standard_name= "ORF L3"
                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "ORF L7"
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                                                                                                                                                                                                                                                                                                                                                                  /gene= "nifD"
                                                             /gene= "dctA'
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      /product- "protein required for nitrogenase activity" complement (441042..441899)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for nitrogenase activity'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'product= "positive regulator of nif, fix and other
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                                                                                                                                                                                                                                                                                                              / Landard_name= "ORE K13"
/product= "ferrodoxin/ferrodoxin-like protein"
/note= "homologous to the FdxN gene"
complement (434753.436234)
                                                                                                                                                                                                                                                                                                                                                                                                /product- "protein involved in FeMo co-factor
                                                                                                                                                                                                                    /product= "protein of unknown function"
/note= "homologous to the FixU gene"
complement (434107..434433)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "ORF K21"
/product= "protein of unknown function"
444337..445029
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complement (434517..434711)
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complement (443313.,443879)
                                                                     /note= "homologous to the GLUD1 gene"
complement (430538..431284)
/product= "transposase homologue"
/note= "homologous to the Tnp gene"
428292..429623
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/note- "homologous to the Tnp gene"
complement (433880..434110)
                                                                                                                   /product="transposase homologue"
complement (431296..432840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene= "fixx"
/product= "protein required
complement (438605..439912)
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complement (436460..438130)
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/standard_name= "ORF Kll"
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/gene= "nifB"
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/standard_name= "ORF K16"
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/gene= "fixB"
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/standard_name= "ORF K22"
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                                                                                                       /standard_name= "ORF K9"
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nucleotide sequence are claimed. The nucleotide sequences or ORFs can be used e.g. in the transportation of compounds to and from an organism which is a host to at least one of the nucleotide sequences, ORFs or proteins, the degradation and/or metabolism of organic, inorganic, natural or xenobiotic substances in a host organism or the modification of the host range, nitrogen fixation abilities; for obtaining a synthetic minimal set of ORFs required for functional Rhizobium-legume symblosis, especially for nodulation efficiency on host plants.
                                                                                                                                                                                                                                                                                                    Db 395468 ACGCACACTCGAGCATTCCGTCATGGACCTCTTTCCCGGCGGCGGTGCAAAAGAAGCATC 395409
                                                                                                                                                                                                                                                                                                                                                                                                                         395291 CGGCTCTGCCCGCGTCATTGCGGACCTGGTATCTGGCCGGAAGCCCGAGATCGACGCCAC 395232
                                                                                                                                                                                                                                                                       ACGCACGCTCGAAAACTTCTTC-CAGCCCTCGCGCCTGCGAGTTCTGAAGAACGATATTC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a Pseudomonas aeruginosa nucleic aicd sequence. P. aeruginosa is an opportunistic human pathogen present in
                                                                                                                                                     Sequence 536165 BP; 111291 A; 155755 C; 157864 G; 111255 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                       395408 CTATTGGTCGGGTCTGCGCCCAATGACGCGGGCGCGCCGTCATCGGCC---CAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1173 GATGACCGCAACGCTCCTCAGAGCTCCTCGCAGGCGAAAAGACCTCAATCGACATTTC
                                                                                                                                                                                                                                                                                                                                     1053 CAAATGGATGGGGTTCCGGCCGAGCATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                    1113 CCGGACACCCGGACGTAATCTATGCTTTCGGCCATGGTCATCTCGGCATGACAGGGGCGCC
                                                                                                                                                                                                     Length 536165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahajan-Miklos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence of ORF33512 encoding a virulence factor
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                    Score 35.4; DB 19;
Pred. No. 4.7;
0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goodman HM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          395231 CGACCTCGCCGTCAGCCGCTACGCT 395207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1233 GCCCTTCGCACCAAACCGCTTTGGT 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 228pp; English.
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                                                                                                                                                                                                    Query Match 2.7%;
Best Local Similarity 50.9%;
Matches 135; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                x98168/c
ID X98168 standard; DNA; 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-357851/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rahme LG,
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                                                                                                                                                                                                                                  Db 395468 ACGCACACTCGACCATTCCGTCATGGACCTCTTTCCCGGCGCGCGAAAGAAGAAGCATC 395409
                                                                                                                                                                                                                                                                                    Db 395408 CTATTGGTCGGGTCTGCGCCCCATGACGCCGGACGGCACGCCCGTCATCGGCC---CAAC 395352
                                                                                                                                                                                                                                                                                                                                                                   395292
                                                                                                                                                                                                                                                                                                                                                                                                                         1113 CCGGACACCCGACGTAATCTATGCTTTCGGCCATGGTCATCTCGGCATGACAGGGGCGCC 1172
                                                                                                                                                                                                                                                                                                                                                                                                  1173 GATGACCGCAACGCTCGTCTCAGAGCTCCTCGCAGGCGAAAAAGACCTCAATCGACTTTC 1232
                                                                                                                                                                                                  994 ACGCACGCTCGAAAACTICTTC-CAGCCCTCGCGCCTGCGAGTTCTGAAGAACGATATTC 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the nucleotide sequence of the plasmid pNGR234a isolated from Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated symbiotic plasmid from Rhizobium sp. NGR234 - used to develop products for modifying plant characteristics, e.g. nitrogen fixation, synthesis of compounds and stress response
                                                                                                                                                                                                                                                                                                                                                       D 395351 GAAGATCGCCGGTCTCTTCCTTAACACCGGGCACGCCACGCTTGGCTGGACGATGAGCTC
                                                                                                                                                                                                                                                                 1053 CAAATGGATGGGGTTCCGGCCGAGCATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAAC
                                                                                                                                    Length 534720;
                                                                                                                                                                     4 ;
                                                               /product="processing protease-like protein"
/note= "homologous to the PP gene"
466590..467021
                                                                                                                                                                     Indels
/note= "homologous to the bI-MPP gene"
464736..466079
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                                                                                                                                                                 0; Mismatches 126;
                                                                                                                                    DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INS'T MOLECULAR BIOTECHNOLOGY.

LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE.
                                                                                                                                  Score 35.4; Di
Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rhizobium species symblotic plasmid pNGR234
                                                   /standard_name= "ORF L15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Frelberg CB, Perret XP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Db 395231 CGACCTCGCCGTCAGCCGTACGCT 395207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1233 GCCCTTCGCACCCAAACCCCTTTGGT 1257
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                                                                                                                                    2.7%;
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                                                                                                                                                                     Conservative
                                  /*tag=
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                                                                                                                                                  Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     legume; plant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rhizobium sp
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                                                                                                                                    Query Match
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V30459/c
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soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. acruginosa infection.

Is a P. acruginosa infections.

In some instances given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a Pseudomonas aeruginosa nucleic aicd sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be
                                                                                                                                                                                                                                                                                                                                                                                                             76 CGCCGCGCGATTCAAAGTCACCTTGATTGACCCGAACCCTCCTGGCGAAGGTGCATCGTTT 135
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                        16 AAAAAAGTAGGCATCGCTGCAGCCGGAATCGTCGCGCGTATGCACGGCGCTGATGCTTCAG 75
                                                                                                                                                                                                                                                                                                                                                                           146 AGAGATGTAGTAGTAGTAGCGCCTGGCGTCATCGGCCTGTTGACCGCCCGGGAGCTGGCG 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                86 CTCCCCCGACTGCCGGTGACCCTGGTGGAGCGGGGCGAGAGTGGGCGTGAGGCATCCTGG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of ORF33205 encoding a virulence factor.
                                                                                                                                                                                                                                                                      Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pathogen; virulence polypeptide; virulence factor;
pathogenic infection; Pseudomonas aeruginosa infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                       65; Indels
                                                                                                                                                                                                                 Seguence 405 BP; 98 A; 135 C; 97 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                    DB 20;
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                                                                                                                                                                                                                                                                                   0.4;
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                  Score 34;
Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 228pp; English.
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                                                                                                                                                                                                                                                                2.6%;
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Fan M, Tsongalis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 GGGAATGCCGGATGCTTC 153
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                                                                                                                                                                                                                                                                                                       73; Conservative
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                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                 correct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           x98167;
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                                                                                                                                                                                                                                                                                                       Matches
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used to treat pathogenic infections, especially where the infection is a P. aeruqinosa infection. note: the sequences given in the specification were poorly legible, and in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                                                                                              394
                                                                                                                                                                                                                                                                                                                76 CGCCGCGGGATTCAAAGTCACCTTGATTGACCCGAACCCTCCTGGCGAAGGTGCATCGTTT 135
                                                                                                                                                                                                                                                                                                                                                 393 creecedeacrecederanceregregadesegedeacandagegegegegegearecereg 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents a Pseudomonas aeruginosa nucleic aicd
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                              16 AAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGCGCGTATGCACGCGCGCTGATGCTTCAG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of ORF33705c encoding a virulence factor.
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                                                                                                                                                                         Score 34; DB 20; Length 603; Pred. No. 0.49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factors useful in developing disease treatments
                                                                                                                                                                                                           Indels
                                                                                                                       Sequence 603 BP; 119 A; 219 C; 1.71 G; 94 T; 0 other;
                                                                                                                                                                                                           65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goodman IIM,
                                                                                                                                                                                         Pred. No. 0.49
0; Mismatches
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Tsongalis J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                         Query Match 2.6%;
Best Local Similarity 52.9%;
Matches 73; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     136 GGGAATGCCGGATGCTTC 153
                                                                                                                                                                                                                                                                                                                                                                                                                      333 GCGGGAGCCGGGATCGTC 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X98164 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virulence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x98164;
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In some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                                    The present sequence represents a Pseudomonas aeruginosa nucleic aicd
                                                                                                                                                                    49 agagatgtagtagtggtaggcgctggcgtcatcggcctgttgaccgcccgggagctggcg 108
                                                                                                                                                                                                  76 CGCCGCGGGATTCAAAGTCACCTTGATTGACCCGAACCCTCCTGGCGAAGGTGCATCGTTT 135
                                                                                                          Gaps
                                                                                                                                       16 AAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACGGCGCGTGATGCTTCAG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goodman HM, Mahajan-Miklos
                                                                       Score 34; DB 20; Length 1137;
Pred. No. 0.67;
0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virulence factors useful in developing disease treatments
                                                                                                       65; Indels
                              Sequence 1137 BP; 173 A; 351 C; 413 G; 200 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of cosmid BI48.
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Tan M, Tsongalis J;
                                                                                                                                                                                                                                                                                                                                        RESULT 15
X98035/c
ID X98035 standard; DNA; 42235 BP.
                                                                          2.6%;
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                                                                                                                                                                                                                                                               136 GGGAATGCCGGATGCTTC 153
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Best Local Similarity 52.9'
Matches 73; Conservative
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Sequence 42235 BP; 9002 A; 13134 C; 12218 G; 7876 T; 5 other;

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                                           Gaps
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2.6%; Score 34; DB 20; Length 42235; 52.9%; Pred. No. 3.9; Live 0; Mismatches 65; Indels 0
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Search completed: January 1, 2001, 03:32:11 Job time: 19539 sec

33537 GCGGGAGGCGGGATCGTC 33520

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FILING DATE: US/08/391,339
FILING DATE: CLASSIFICATION: 800
                     US-09-144-759-19

US-09-144-759-19

US-09-104-759-21

US-08-9-028-931-1

US-08-469-537A-104

US-08-469-986-1

US-08-461-147-3

US-08-441-147-3

US-08-440-8450-8

US-08-440-8450-8

US-08-474-177-1

US-08-480-810-1

US-08-480-810-1

US-08-480-810-1

US-08-480-810-1
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITX: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-848-251-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: HOETNET, DENTIS R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(1)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5463175
GENERAL INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: HOETNEY, DennIS R.
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STRANDEDNESS: double
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Sequence 3,
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'CgnZ_6/ptodata/2/ina/pcTuS_COMB.seq:*
                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-391-339-6
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                                                               CCGGATTCGCTCCCCGTGATTGGCCGGGCAACCCGGACGACGTAATCTATGCTTTC
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REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
TELECOMMUICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTY: USA

ZIP: 77210-4433

COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIA-
COMPUTER: IBM PC COMPALIA-
COMPUTER: IBM PC COMPALIA-
COMPUTER: IBM PC COMPALIA-
COMPUTER: DATEM: PC-DOS/MS-DOS
SOFTWARE: PAEGNIN PRESENCE #1.0, Version #1.
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                            100.0%; Score 1293;
100.0%; Pred. No. 0;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Durkee
                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08484274A Patent No. 5776760 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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LOCATION: 1..1
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US-08-484-274A-4
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Matches 1293;
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               Length 1293;
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           Score 1293; Pred. No. 0; Mismatches
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Best Local Simi
Matches 1293;
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ADDRESSEE: Dennis R. Hoerner, ADDRESSEE: Monsanto Co. BB4F
                                                                                                                                            Sequence 3, Application US/08391339 Patent No. 5463175
                                                                                                                                                                         APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hoerner, Dennis R., JI
REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
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US-08-391-339-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (314)537-6099 INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1293; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                         CITY: St. Louis
STATE: Missouri
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                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                             USA
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STREET: 70
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  GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC
                                                                                 ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGGCCGTTGTCAA
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                                                                                                                                                                                                                                                                              Tolerant Plants
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                    GGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1293
                                                                                                                 700 Chesterfield Village Parkway
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Pred. No. 0;
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CLASSIETCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/717,370
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                                                TCCGGTTCAGCTATTTCCAACCATCATGCCTGGTTGATTCGCTTTCTGTTAGCCCGGAAGA
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CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: PALTERSON, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBIL30 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: O7 June 1996
CLASSIFICATION: 435
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              1380 GGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1412
                                                                                                                                                                                  Tolerant
                                                                                                                                                                                                                             Durkee
                                                                                                                                                                                                                                                                                                  ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                     Sequence 3, Application US/08484274A Patent No. 5776760
                                                                                                                                                 APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate
UNMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Du
                                                                                                                                                                                                                           E: Arnold, White & P.O. Box 4433
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99.8%;
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Best Local Similarity 99.8
Matches 1293; Conservative
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                                                                                                                                                                                                                                                           Houston
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                                                                                     US-08-484-274A-3
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                  CCTCTGATCAAGTCATTGGCGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT
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Patent No. 5463175
GENERAL INFORMATION:
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Kishore, Ganesh M.

APPLICANT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                           Version #1.25
              Glyphosate Tolerant Plants 33
                                                          STREET: 700 Chesterfield Village Parkway CITY: St. Louis STATE: Missouri COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.1%; Score 1255.2;
99.5%; Pred. No. 0;
ilve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           38-21(10533)
                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
FILING DATE:
CLASSIFICATION: 800
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
FILING DATE:
APPLICATION NUMBER: US/08/156,368
                                                                                                                                                                                                                          Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hoerner, Dennis R., Jr. REGISTRATION NUMBER: 30,914
                                                                                                                                                       ZIF: 0-1.0.
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Hoerner, Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (314)537-6099 INFORMATION FOR SEQ ID NO: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
 Gerard
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Matches 1290; Conservative
                                                        ADDRESSEE: Dennis R. ADDRESSEE: Monsanto C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double
                                          CORRESPONDENCE ADDRESS:
APPLICANT: Barry, Ge
TITLE OF INVENTION: ONUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
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                                                                                                                                                 63198
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FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT 107 June 1996
TATORNEY/AGENT INCHMATION:
NAME: Patterson, Mellinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBTI30 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                    COMPUTER READABLE FORM:
                                     77210-4433
  Houston
                 Texas
                                                                MEDIUM TYPE:
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                          COUNTRY:
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                                                   CGGCGTCTCAACGGTGTTCGCACGCAGGTCCTCAGCGCCGGTGCGTTGCGGGATTTCGAT
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Patent No. 5776760
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                                                          1 ATGTCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG
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                                                                                                                                     Length 1296
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                              3;
 DB
Score 1255.2;
Pred. No. 0;
0; Mismatches
97.1%;
ilarity 99.5%;
Conservative
              Best Local Similarity
Matches 1290; Conserv
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GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate TO
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: ARNOLd, White & Durk
STREET: P.O. Box 4433

3: Arnold, White & Durkee P.O. Box 4433

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GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC 180
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                                                                                                                                                                                                                                                       89.8%; Score 1160.8; 95.0%; Pred. No. 0;
                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                             38-21(10533)
                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/117,370
FILING DATE:
ATOGENT INFORMATION:
NAME: HOGENET, DEGNIS R., Jr.
                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (recombinant) US-08-391-339-7
                                                                                       NAME: HOERNEY, DENDIS R., JI
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6699
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
                                                                                                                                                                                                                                                                            Matches 1231; Conservative
                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                   Best Local Similarity
  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                         Query Match
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 700 Chesterfield Village Parkway CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant INMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. BB4F
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPRERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/484,274A FILING DATE: 07 June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT
TELECOMMUNICATION INFORMATION:
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0; Mismatches
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                                                                                     MOLECULE TYPE: DNA (recombinant)
(713)789-2679
SEO ID NO: 7:
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95.0%;
           INFORMATION FOR SEQ 1D NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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  TELEPHONE:
                                                                          TOPOLOGY:
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                         GCGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA
                                                                                                                                                                                                                                                                                              Sequence B, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION
APPLICANT: Rishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1...
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
FILING DATE:
                                                                                                                                                                                                                                                                                                                                    ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1293
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38-21(10533)
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APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(1)
TELECOMUNICATION INPORMATION:
TELEPHONE: (314)537-6099
INPORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
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ZIP: 63198
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STRANDEDNESS:
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                                          Length 1296;
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                                        Score 928.8; DB 1;
Pred. No. 0;
0; Mismatches 207;
; MOLECULE TYPE: DNA (synthetic) US-08-391-339-8
                                         Query Match 71.8%;
Best Local Similarity 83.8%;
Matches 1086; Conservative
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
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NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                            & Durkee
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                ; Sequence 8, Application US/08484274A
; Patent No. 5776760
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83.8%;
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Best Local Similarity 83.8
Matches 1086; Conservative
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ADDRESSEE: Arnold, W
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STRANDEDNESS: double
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ZIP: 77210-4433
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                                                                                    TTCGGCCATGGTCATCTCGGCATGACAGGGGCGCCGATGACGCCGCAACGCTCGTCTCAGAG
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                                                                                                                                                                           1258 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 700 Chesterfield Village Parkway CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Hoerner, Dennis R., Jr.
REGISTRATION UNUMBER: 30,914
REFERENCE/DOCKET UNUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (344)537-6099
INFORMATION FOR SEO ID NO: 17:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Dennis R. Hoerner, Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                Sequence 17, Application US/08391339 Patent No. 5463175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (recombinant)
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83.68;
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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US-08-391-339-17
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Best Local Simi
Matches 1084;
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                                                                                                                                                                                                                         COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TBM PC COMPALIBLE

COMPUTER: TBM PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,274A

FILING DATE: 07 June 1996
                                                                                                                                                                                                                                                                                                       FILING DATE: ...
FILING DATE: ...
FILING DATE: ...
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATCESSON, MOBINGAL.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: Acouble
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83.6%; Pred. No. 0;
iive 0; Mismatches 209;
                                                                                                                                     APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                 1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                      1258 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1293
                                                                                                                                                                                     E: Arnold, White & Durkee P.O. Box 4433
                                                                                                         Sequence 17, Application US/08484274A
Patent No. 5776760
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Matches 1084; Conservative
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                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                             STREET: P.O. BC
CITY: Houston
STATE: Texas
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                                                                                                                                                                                      ADDRESSEE:
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US-08-484-274A-17
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AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
                                                            418 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGGGGGGGTTGGGAACTG
                                                                                                                                                                                                                                           538 CCGAACTTGTCGCATGCGTTTACCAAGGGCATTCTTATAGAAGAACGGTCACAGATT
                                                                                                                                                                                                                                                                                          598 AATCCGCAAGGCTCGTGACCCTCTTGTTTCGCGTTTTATCGCGAACGGTGGCGAATTC
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Length 69;
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                               COUNTRY: 1638

21P: 77210-4433

COUNTRY: USA

SID: 77210-4433

COMPUTER READABLE FORM:
MEDIOW TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: PATCESON, MAINDA L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBTI30 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTER STICS:
LENGTH: 69 base pairs
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
TYPE: NUCLEIC SINGLE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11arity 88.4%; Score 56.2; DB 2; Secretity 88.4%; Pred. No. 9.4e-10; Conservative 0; Mismatches 8;
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/717,370 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/08391339 Patent No. 5463175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (synthetic)
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Best Local Similarity
Matches 61; Conserva
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Houston
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US-08-391-339-33
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SOUUNCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                   APPLICANT: Rishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE: Dennis R. Hoerner, Jr.,
ADBRESSE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38-21(10533)
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
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APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: HOERNEY, Dennis R., Jr.
RECISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314,537-609)
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                                        Sequence 30, Application US/08391339 Patent No. 5463175 GENERAL INFORMATION:
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Best Local Similarity 88.45
Matches 61; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
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STATE: Missouri
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Gaps ö

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ATTORNEY/AGENT INFORMATION:

NAME: HOGTNEY, Dennis R., Jr.

REGISTRATION NUMBER: 30,914

REFERENCE/POCKET NUMBER: 38-21(10533)

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 69 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TYPE: nucleic acid

TYPE: nucleic acid

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

NOCOLOGY: linear

US-08-391-339-33
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ó 0; Gaps Ouery Match 4.2%; Score 54.6; DB 1; Length 69; Best Local Similarity 87.0%; Pred. No. 3.3e-09; Matches 60; Conservative 0; Mismatches 9; Indels

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61 TCTCGTCTC 69

Search completed: January 1, 2001, 03:17:38 Job time: 29282 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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Perfect score:
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117:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES æ

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AUTHORS TITLE JOURNAL COMMENT REFERENCE

Direct Submission
Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CBiO 15A, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk
see http://www.ebi.ac.uk/parasites/leish.html
Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/
The primer sequence can be obtained from alicat@sanger.ac.uk. Oryza sativa
Cryza sativa
Cryza sativa
Eukaryota: Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; Liliopsida; Poales; Poaceae; Oryza.

I (bases 1 to 702)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University Genomics Institute ö Leishmania. 1 (bases 1 to 434) Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and P149R 434 bp DNA GSS 16-MAR-2000 Leishmania major Friedlin PAC P149 right end-sequence, genomic 297 GTTCTTGTCGATCGCGCGCGCGCGCACCGAGCCTCCTATGCCAACGCGGCTTCATC 238 94 ACCTTGATTGACCCGAACCCTCCTGGCGAAGGTGCATCGTTTGGGAATGCCGGATGCTTC 153 AQ328054 702 bp DNA GSS 08-JAN-1999 nbxb0042102f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0042102f, DNA sequence.
AQ328054 GI:4119904 Gaps 34 GGAGCCGGAATCGTCGGCGTATGCACGGCGCTGATGCTTCAGCGCCGCGGATTCAAAGTC 93 98146435 2 (bases 1 to 41) Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Leishmania major. Leishmania major Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; ö Length 434; Smith, D.F. A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998) 76; Indels 3.4%; Score 44.4; DB 124; 54.2%; Pred. No. 0.02; tive 0; Mismatches 76; /organism="Leishmania major" /strain="Friedlin" /db_xref="taxon:5664" /clone="PAC P149" AL160534.1 GI:7258935 Best Local Similarity 54.2 Matches 90; Conservative survey sequence. AL160534 Oryza sativa. Barrell, B.G. 92 Query Match RESULT 2 AQ328054/c ACCESSION VERSION KEYWORDS SOURCE ORGANISM source LOCUS BASE COUNT ORIGIN LOCUS DEFINITION ORGANISM TITLE JOURNAL JOURNAL REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS FEATURES TITLE COMMENT ð qq ò g ö

> Н RESULT P149R/c

ALIGNMENTS

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/db.xref="taxon:54126"
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/dev_stage="mixed stages (embryo to adult)"
/dab_host="not applicable (host cell line)"
/note="Vector: Uni-249 KR Vector (Stratagene); Site_1: 5'
EcoRI; Site_2: 3' XhoI; lst strand cDNA was primed with a
XhoI - oligo(dT) primer. Double-stranded cDNA was ligated
to EcoRI adaptors digested with XhoI and cloned into XhoI
and EcoRI sites. Primary complexity of the library was 10
in the 7th, The library went through one round of
, Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas McCann, R., Waterston, R. and Wilson, R. Washington Univ. Nematode EST Project, 1999
                                                                                                                                                                                                                                                                                            Email: estewatson wustl.edu
The library was constructed by Dr. Ralf Sommer DNA Sequencing by:
Washington University Genome Sequencing Center
Contact Dr. Ralf Sommer (talf.sommerêtuebingen.mpg.de) for
information about this clone.
Seq primer: -40RP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                       Unpublished (1999)
Contact: McCarter JP
Contact: McCarter JP
Washington University School of Medicine
Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 CGCCGAACCTCGTNNGCCGAAATCGCNNTACTCATTGNNGAACCACTTCCATTCTTNNGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Pristionchus pacificus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 2.8%; Score 36.4; DB 19; Best Local Similarity 45.1%; Pred. No. 5.3; Matches 97; Conservative 0; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH-MGC http://www.ncbi.nlm.nlh.gov/MGC/.
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Location/Qualifiers
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AW500960.1 GI:7114040
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                                                                                                                                                                                                                                                                                                            /cultivar="Nipponbace"
/db_xref="taxon:4530"
/clone="nbx0042102f"
/clone="nbx0042102f"
/clone="nbx0042102f"
/clone="nbx0042102f"
/clone="nbx0042102f"
/clone="type="Leaf"
/lab_host="E. coll DH10B"
/note="Vector: pBeloBAC11: Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library from Oryza sativa, Nipponbare variety. The cep coverage allows the isolation a particular sequence with a probability of 99.9% . Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
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McCarter,J., Clifton,S., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     375 GCCGCAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            435 TGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTGCGGCGTCTCAACGGTGT 494
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.9%; Score 37.4; DB 96; Length 702; 53.0%; Pred. No. 2.7; 11 Indels 0
                           Clemson, SC 29634, USA
             100 Jordan Hall, Clemson, SC 29634, Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAMTACGACTCACTATAGGG
Class: BAC ends
High quality sequence stop: 365.
Location/Qualifiers
                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
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Matches 80; Conserv
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                                                                                                                                                                  FEATURES
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/organism="Homo sapiens"
/ob_xref="taxon:9606"
/clone="IMAGE:3073464"
/clone=lib="NHE_MGC_51"
/tissue_type="germinal center B cells"
/cell_line="MGCB5"
/cell_line="mGCB5"
/cell_line="germinal center B cells"
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/cell_l
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
                                                        Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Eco RI stee shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
COne distribution: M.G. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.lln|gov/bbrp/image/image.html
Seq primer: Ml3 Forward.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     378 CGGGTGCATGCCTTCCCGACGACGACGGATCGATCGCGATGAAATGCCCGACGGAGGTG 319
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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50.0%; Pred. No. 6.1;
tive 0; Mismatches
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1. .380
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AW501280.1 GI:7114663
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Matches 90; Conserv
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Actinopterygii; Neopterygii; Teleostei; Etteleostei; Neoteleostei; Etteleostei; Etteleostei; Etteleostei; Etteleostei; Etteleostei; Etteleostei; Etteleostei; Etteleostei; Etteleostei; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoldei; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Tetraodontidae; Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Tetraodon nigroviridis genome survey sequence SP6 end of clone
027A06 of library B from Tetraodon nigroviridis, genomic survey
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortlum/LLNL at:
www.blo.llnl.gov/bbr/image/image.html
Seq primer: MI3 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGTCAT 420
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Rocest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fishe
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 CTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTGCGG
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                                                                                                                                                                                                                                  /db_xref="taxon:9606"
/clone="IMAGE:3073186"
/clone_lib="NIH_MGC_51"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 36; DB 22;
50.0%; Pred. No. 6.1;
tive 0; Mismatches 90;
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/organism="Homo sapiens"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCCACAGG 3' -3' adaptor sequence: CTCGAGITITITITITITITI 3' "
59 c 52 9 67 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .360
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105 c 109 g
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Best Local Similarity 53.2%;
Matches 74; Conservative (
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Contact: Yuji Kohara
Gene Library Lab
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/clone="IMAGE:845450"
/clone="Lib="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="Ncl H69"
/dev_stage="cell line NCI-H69"
/nab_nost="SOLR (kanamycin resistant)"
/note="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI
/site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT. Small cell carcinoma cell line NCI-H69. Average
                   Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis qenome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 226)

Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., Washle,T., Waller,T., Waterston,R. and Wilson,R.

Unpublished (1997)

Contact: Wilson RK
                                                                                                                                                                                                                                               : COAB027BA03B2~end : SP6"
25 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL : contact the
IMAGE Consortlum (info@image.llnl.gov) for further information.
Insert Length: 716 Std Error: 0.00
Seg primer: -40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                            967 AACTGGAAACGTGCGCATGTGCTCTATACGCACGCTCGAAAACTTCTTCCAGCCCTCGCG 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        538 AATTGGCAAAAAGAACAAGTNCTTTATCATCTCCCTCGAAAACTTCCACCAGCTGCTGCT 597
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 123; Length 895;
Pred. No. 7.6;
0; Mismatches 53; Indels
                                                                                                                                                                /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="027806"
/roote="Genescope sequence ID : COA
216 c 182 g 227 t 25
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Best Local Similarity 55.5%;
Matches 66; Conservative (
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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidaes; Peloderinae; Caenorhabditis.

1 (bases Lo 360)
Kohara,Y., Shin-1,T., Thierry-Mieg,J., Thierry-Mieg,D., Mitsuki,H., Nishigaki,A., Motohashi,T., Zeng,O., Watanabe,H., Sugimoto,A., Sano,M., M., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and
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AV190084 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk566f3 5', mRNA sequence.
AV190084
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624 GITTCGGCGTTTTATCGCGAACGGTGGCGAATTCGTATCTGCGCGTGTCATCGCTTTGA 683
                                                 Gaps
                                                                                                                        unpublished cDNA:Strain N2
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  Length 226;
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/strain="N2"
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/ Match 2.7%; Score 35.4; DB 5;
Local Similarity 57.8%; Pred. No. 8.1;
nes 63; Conservative 0; Mismatches 46;
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Yata 111, Mishima, Shizuoka 411, Japan
Trel: 81-559-81-6854
Fax: 81-559-81-6855
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0; Mismatches
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/clone_lib="Yuji Kohara
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house mouse.
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                                                                                                                                                                                                                             Eukaryota; Metazoa; Ummatoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

; Rhabditidae; Peloderinae; Caenorhabditis.
; Rhabditidae; Peloderinae; Caenorhabditis.
; Kohara,Y., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano, M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
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                                                                                              C47876 382 bp mRNA ESI 10 C47876 Yuji Kohara unpublished CDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans CDNA clone yk453a5 5', mRNA sequence.
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Chlamydomonas reinhardtii
Eukaryota; Viridplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 517)
Asamizu.E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV386799 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii CDNA clone CM007a05_r, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 GACGCAGGTCTCCATCTGCGTCGAAGAGCCCCCGCCGCAGCGAGAAGACGCGCTCCACCAT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unpublished cDNA:Strain N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Caenorhabditis elegans"
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/clone="yk453a5"
/clone_lib="Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
a 112 c 116 g
                                                                                                                                                                                                   Caenorhabditis elegans.
Caenorhabditis elegans
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/strain="N2"
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                                                                                                                                                                 C47876.1 GI:2384129
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Best Local 8
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AV386799
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                                                                                                                  DEFINITION
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Matches
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KEYWORDS
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A Large Scale Structural Analysis of cDNAs in a Unicellular Green Alga, Chlamydomonas reinhardtii. I. Generation of 3433
Non-redundant Expressed Sequence Tags
Non-redundant Expressed Sequence Tags
DNA Res. 6, 369-373 (1999)
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Kazusa DNA Research Institute
Sazusa DNA Research Institute
Email: ynakamu@kazusa.or.jb, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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AV316270 RIKEN full-length enriched, adult male thymus Mus musculus
CDNA clone 5830435F07 3', mRNA sequence.
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Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishikawa,T., Itch,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Owa,C., Ozawa,Y., Saito,H., Sano,M., Saro,K., Shibata,X., Shipara,A., Yoshino,M., Muramatsu,M., and Hayashizaki,Y., Yoshino,M., Muramatsu,M., and Hayashizaki,Y., Shibara,A., Shibara,A., Shipara,A., Shipara,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 171)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CM007a05_r"
/clone_lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptii SK-; Site_l: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Science Laboratory
The Institute of Physical and Chemical Research (RIKEN), Genomic
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Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318 GCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGC 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 GCTGACGGACGTGCTGCGCGAGATCATCAAGCCCGAGGCCCCCCAGCACAACTTCAAGCG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 GGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCGTGG 437
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Pred. No. 13;
0; Mismatches 120; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Chlamydomonas reinhardtii"
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/db_xref="taxon:3055"
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Best Local Similarity 47.1%;
Matches 107; Conservative
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Lotus japonicus
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bugnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Eabales; Pabaceae; Papilionoideae; Lotus.
I (bases I to 205)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ŋanakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta, eudicotyledons; core eudicots, Rosidae, eurosids I;
Fabales; Fabaceae, Papillonoideae; Lotus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               // Corganism="Lotus japonicus"
/organism="Lotus japonicus"
/ob_xref="taxon:3436s"
/clone="mwMx32a12_r"
/clone="mwMx32a12_r"
/clone="mwmx32a12_r"
/clone="mwmx32a12_r"
/clone="mwmx32a12_r"
/note="weetor: pBluesoriptII SK-; Site_1: EcoRI; Site_2: xhoI: isolate=Miyakojima MG-20"
xhoI: isolate=Miyakojima MG-20"
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AV418303 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM155h01_r 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 2.7%; Score 34.8; DB 18; Length 205; Best Local Similarity 58.8%; Pred. No. 12; Matches 60; Conservative 0; Mismatches 42; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Lotus japonicus"
/db_xref="taxon:34305"
/clone="MWM155h01_r"
                                                                                                                                                                                                                                                                                                                     legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
20277479
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DNA Res. 7 (2), 127-130 (2000)
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Contact: Yasukazu Nakamura
   AV413471.1 GI:7742647
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                                                                  Lotus japonicus.
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MEDLINE
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                                                                                                                                                                                                                                                            AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
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//dev.stage="adult"
//de
                                                                                                                       Email: genome-resértc.riken.go.jp,
URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matguura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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65.4%; Pred. No. 11;
tive 0; Mismatches 27; Indels 0.
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                       3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
Fax: +81-298-36-9098
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Matches 51; Conserv
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El (bases 1 to 271)

S Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics of the contact: Udvardi MK
Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250

Email: udvardi@mpimp-golm.mpg.de
Seq primer: T7
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0
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev.stage="young plants (two-week old)"
/note="vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhol; Isolate=Mpakojima MG-20"
76 c 55 g 59 t
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//dev_stage="5 and 7 week-old plants"
//note="Organ: Nodule; Vector: pSPORT1; Site_1: Sall;
Site_2: Not1; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
strain R7A."
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/organism="Lotus japonicus"
/cultivar="Gifu (8-129)"
/db_xref="taxon:34305"
/clone_lib="Lotus japonicus nodule library 5 and 7
week-old"
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58.8%; Pred. No. 13;
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Location/Qualifiers
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                                                                                                                                  2.7%;
llarity 58.8%;
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Lotus japonicus
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Best Local Simi
Matches 60;
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4 TCTGAGAACCACAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACGGCG 63

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E. 'Course', remundance, reptillolluede; Lotus.
S. Asamizu, E. 'Lota's 1 to 273 and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
L. DNA Res. 7 (2), 127-130 (2000)
E. 2027479
Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamukazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
Free 1. 273
                                                                                                                                                                    Lotus japonicus.
Lotus japonicus
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.
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/dev_stage="young plants (two-week old)"
/note="yoctor: pBluescriptII SK-; Site_l: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
91 c 47 g 72 t
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AV427698 273 bp mRNA EST 23-MAY-2000 AV427698 Lotus japonicus young plants (two-week old) Lotus japonicus cona clone MW085c02_r 5', mRNA sequence. AV427698.1 GI:7787904
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/db_xref="taxon:34305"
/clone="MWM085c02_r"
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58.8%;
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Best Local Similarity 58.87
Matches 60; Conservative
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR016593 Sequence	Il5326 Sequence 6	AR016591 Sequence	AR016592 Sequence	I15325 Sequence 4	I15324 Sequence 3	AR016594 Sequence	I15327 Sequence 7	AR016595 Sequence	I15328 Sequence 8	AR016604 Sequence	115337 Sequence 17
SUMMARIES	AR016593	I15326	AR016591	AR016592	115325	I15324	AR016594	11.5327	AR016595	115328	AR016604	115337
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a Query Match Length DB, ID	1296	1296	1692	1293	1293	1689	1296	1296	1296	1296	1296	1296
& Query Match	100.0	100.0	9.66	6.96	96.9	96.9	92.7	92.7	74.2	74.2	74.0	74.0
Score	1296	1296	1291.2	1255.2	1255.2	1255.2	1201.6	1201.6	961.6	961.6	958.4	958.4
Result No.	٦.	7	e	4	ស	Q	7	80	O	1.0	11	12

Db 121 GAAGGTGCATCGTTTGGGAATGCTGGACGGCTCATCCGTCGTCGTCCTATGTCC 180	Qy 241 ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGA 300	OY 301 AGACCAAACATGAAGGAGCAGAGAAGCACTCCGCAATCTCATCAAGTCCACGTG 360	Oy 361 CCTCTGATCAAGTCATTGGCGGAGGAGCTGATGCGAGCCATCTGATCCGCCATGAAGGT 420	QY 421 CATCTGACCGTATATCGTGGAGAACTACGCCAAGGACCGGGGGGGG	Oy 481 CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCAGCGCCGATGCGTTGCGGGATTTCGAT 540	OY 541 CCGAACTTGTCGCATGCGTTTACCAAGGCCATTCTTATAGAAGAACGGTCACAGGTT 600 	QY 601 AATCCGCAAGGCTCGTGACCCTCTTGTTTCGCGGTTTTATCGCGAACGGTGGCGAATTT 660	OY 661 GTATCTGCGCGTGTCATCGGCTTTGAGACGTGGGGGGCGCTTAAAGGCATTACAACC 720	QY 721 ACGAACGCGTTCTGGCCGTTGATGCAGCGGTTGTCGCAGCCGGCGCACTCGAAATCA 780	Qy 781 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC 840	OY 841 ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACCGATGCGTCAGGAAAATTCATC 900	Oy 901 GCGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGGGTTGGGTGGG	QY 961 GCCGCTCCTAACTGGAAACGTGCGCATGTGCTCTATACGCACGC	OY 1021 GCCTCGCGCGGGGTTCTGAAGAACGATATTCCAAATGGATGG	Qy 1081 ATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAACCCGGACGCCGACGTAATCTATGCT 1140	Qy 1141 TTCGGCCACGGTCATCGGCATGACAGGGCGCCGATGACGCAACGCTCGTCTCAGAG 1200	OY 1201 CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGT 1260
A59869 Sequence 1 M69158 Pseudomonas M601616 Sequence I15340 Sequence 30 I15352 Sequence 30 I15352 Sequence 30 I15354 Sequence 31 I15350 Sequence 28 U17017 Ectothiorho AR016617 Sequence I15346 Sequence 21 I15346 Sequence 27 AR016618 Sequence 27 AR0164957 Streptomy L78820 Myrobacteri AC033443 Glardia in AC04957 Streptomy L78820 Myrobacteri AC0318 Angullia an AE000097 Rhizoblum A724919 Rhizoblum A724919 Rhizoblum A724919 Rhizoblum A724919 Rhizoblum A52879 Mille mRNA AE002359 Neisseria AC055863 Homo sapi									PAT 05-DEC-1998					DB 5; Length 1296; 0: Indels 0: Gans 0:	090	C166C1	4 ~
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AATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCCTTTTATCGCGAACGGTGGCGAATTT
                                                               ACGAACGCCGTTCTGCCCGTTGATGCAGCGGTTCGCAGCCGGCGCCACACTCGAAATCA
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Barry,G.Francis and Kishore,G.Murthy.
Glyphosate tolerant plants
Patent: US 5776760-A 3 07-JUL-1998;
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Pred. No. 0;
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Sequence 3 from patent
AR016591 GI:3972868
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Matches 1293; Conservative
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100.0%; Pred. No. v,
0; Mismatches
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 6 31-OCT-1995;
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                                                                     115326 1296 bp DNA
Sequence 6 from patent US 5463175.
115326 11:1250234
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368 c 361 g
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Best Local Similarity 100.
Matches 1296; Conservative
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TITLE
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Db 1200 Qy 1141 Db 1260 Qy 1201 Db 1320 Qy 1261 Db 1380	RESULT 4 ARO16592 LOCUS DOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOUIC BASE COUNT ORIGIN QUELY MA BEST LOC	Match	Db 61 Qy 121 Db 121 Qy 181	0y 241 Db 240 Qy 301	Oy 361 Oy 361 Oy 421 Oy 481
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	41 ATCCGGTTCAGCTATTTCCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGA 30 1111111111111111111111111111111111	540 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGAGGTTGGGAACTG 599 481 CGGCGTCTCAACGGTGTTCGCACGAGATCCTCAGCGCCGATGCGGGATTTCGAT 540 111111111111111111111111111111111111	C 77	21 ACGAACGGCGTTCTGGCCGTTGATGCAGCGGTTGTCGCGCGCCGCGCACACTCGAAATCA	C 900 C 101 C 101 A 960	GCGGCTCCTAACTGGAAACGTGGCATGTGCTATACGCAGCTCGAAACTTCTTCCA 102
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ATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAACCCGGACACCCGGACGTAATCTATGCT 1259 180 ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGGGCCGTTGTCA 240 239 AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360 CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCAGCGCCGATGCGGTTGCGGGATTTCGAT 540 357 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGGGGGTTGGGAACTG 480 Gaps 9 9 05-DEC-1998 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGT 3, DB 5; Length 1293; 3; Indels PAT ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296 1 (bases 1 to 1293)
Barry, G.Francis and Kishore, G.Murthy, Glyphosate trolerant plants
Patent: US 5776760-A 4 07-JUL-1998;
Location/Qualiflers
1. 1293 Similarity 99.5%; Score 1255.2; Similarity 99.5%; Pred. No. 0; 0; Conservative 0; Mismatches 281 AR016592 1293 bp DNA Sequence 4 from patent US 5776760. AR016592 GI:3972869 /organism="unknown" 367 c 359 g б Unknown. Unclassified. 286 a Unknown cal Simi s 1290; çe z Σ

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BASE COUNT 286 a 367 c 359 g 281 t ORIGIN		Db		Oy 541 CCGAACTTGTCGCATGCGTTTACCAAGGCATTCTTATACAAGGGAACGGTCACGCATT 600	Qy 721 ACGAACGGCGTTCTGGCCGTTGATGCGGCGCGCGCGCGCCACTCGAAATCA 780
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Pred. No. 0;
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Barry, G.F. and Kishore, G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 7 31-OCT-1995;
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Best Local Similarity 95.4%;
Matches 1237; Conservative
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Barry,G.Francis and Kishore,G.Murthy
Glyphosate tolerant plants
Patent: US 5776760-A 7 07-JUL-1998;
Location/Qualifiers
1. 1296
                                                                                                    Score 1201.6;
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Best Local Similarity 95.4%;
Matches 1237; Conservative
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ity 83.9%; Pred. No. 9.5e-248;
servative 0; Mismatches 209;
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Francis and Kishore, G.Murthy.

tte tolerant plants

US 5776760-A 8 07-JUL-1998;

Location/Qualifiers
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1296 bp DNA
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ATACGCACGCTCGAAACTTCTTCCA 1020 ACACTCACGCTCGTAAGTTGCTTCCA 1020 CAAGTGGATGGTTTCCGTCCAAGC 1080 CCCGTACTCCAGACGTTATCTACGCT 1140 GATGACCGCAACGCTCGTCTCAGAG 1200 420 240 360 CCAAGGACCGCGGAGGTTGGGAACTG 480 540 TTATAGAAGAGACGGTCACACGATT 600 STACGGTTGAGTTCGCTGGGCTCACA 960 300 CCGCAATCTCATCAAGTCCACGGTG 360 540 STTTCATCGCTAACGGTGGAGAGTTC 660 CGCAGCGGCGCACACTCGAAATCA 780 CTTGATTGATCCAAACCCACCAGGT 120 999 720 TACCGAACGTGGATATCATATCGTC 840 GTTGATTCGCTTTCTGTTAGCCGGA CCTTGACCCGATGGGGCCGTTGTCA GAGCCATCTGATCCGCCATGAAGGT STTTTATCGCGAACGCTGGCGAATTT STAGGGCGCTTAAAGGCATTACAACC CAAATGGATGGGGTTCCGGCCGAGC CCGGACACCCGACGTAATCTATGCT å

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Pred. No. 6.9e-247;
0; Mismatches 211;
                                    1261 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
                                            1 (bases 1 to 1296)
Barry, G.Francis and Kishore, G.Murthy
Glyphosate tolerant plants
Patent: US 5776760-A 17 07-JUL-1998;
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83.7%;
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Matches 1085; Conservative
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                              1081 ATCCCGGATTCCCTTCCAGTGATTGTCGTGCTACCCGTACTCCAGACGTTATCTACGCT
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1 (bases 1 to 1296)

Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 17 31-4
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Length 1296;

DB 5;

Score 958.4;

74.0%;

Db 1021 GCTCTGCCTCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCGGTCCAAGC 1080	RESULT 13 A59869 LOCUS LOCUS DEFINITION Sequence 1 from Patent W09706269. ACCESSION A59869 VERSION A59869.1 GI:3715060 KEYWORDS SOUNCE Arabidopsis sp. ORGANISM Arabidopsis sp. ORGANISM Arabidopsis sp. ATHORS 10 (bases 1 to 1631) AUTHORS 10 (bases 1 to 1631) AUTHOR 10 (bases 1 to 163	tch 67 8%; Score 878.8; al Similarity 80.2%; Pred. No. 1.7 1079; Conservative 0; Mismatches ATGGCTGAGAACCACAAAAAGTAGCATCGTGGAG
Best Local Similarity 83.7%; Pred. No. 6.9e-247; Matches 1085; Conservative 0; Mismatches 211; Indels 0; Gaps 0;	241 241 301 361 361 421 481 481	Db S41 CTAACTYGTCCCCCCTTTTACCAAGGGATCCTTTATCAAGAGGACGGTCCATC COO

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                                                                                                                        TATAGAAGAAGGGTCACACGATTAATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCG
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BCT 26-APR-1993 semialdehyde dehydrogenase

PSEAKSD 3430 bp DNA Pseudomonas putida alpha-ketoglutarate gene, complete cds.

LOCUS

PSEAKSD

RESULT

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1 (bases 1 to 3430)
Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
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                                                                             subdivision; Pseudomonas group;
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                                                                                                                                                                                                                                                               /gene="ketoglutarate semialdehyde dehydrogenase"
603. .2180
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/gene="ketoglutarate semialdehyde dehydrogenase"
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Pred. No. 9.1e-19;
0; Mismatches 602; Indels
                             ketoglutarate semialdehyde dehydrogenase
Pseudomonas putida DNA.
                                                                                                                                                                                                                              /organism="Pseudomonas putida"
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                                                                                                                                                                                                                                                                                                                                                   /product="ketoglutarate s
/protein_id="AAA25698.1"
/db_xref="GI:150982"
                                                                              gamma
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Location/Qualifiers
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1140 c 1157 g
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                                                                             Bacteria; Proteobacteria;
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               GI:150981
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Matches 546; Conservative
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                                                               Pseudomonas
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Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
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Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
gene, complete cds.
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                                           ACGCAGATCCTCAGCGCCGATGCGTTGCGGATTTCGATCCGAACTTGTCGCATGCGTTT
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Pseudomonas putida (strain ATCC 12633) DNA.
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MLTPGIFSAYENGVETLAENTHAQTVAVGRAAKREPVPGTPVRHPGSGFSGECALQAE
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NGWPTGVEVCDAWVHGGPFATSDARTTSVGTAAILRFLRPVCYQDFPDTLLPAALQH
GNPLQLRRLLGRRETCPTRNELTTT"

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EQACALAWAREDRYRETSLATRAEFLETIARETEALGDELIDRAVAETGLPRARILGE
RGRTCQQLRTFPARTVRAGEMLDVRYDAALPERQPLPRADLFRORDIALGPVAVEGASNF
PLAFGSVAGGDTASAAGCPVVKKAHSAHPGTSELVGRAVARNVGKSALPEGYESLLF
GSGREVGIALVSDPRIKAVGFTGSRSGGMALINAAQARLEPIPVYAEMSSINPVLLFP
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/db_xref="G1:151318"
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                                                             /db_xref="taxon:303"
/strain="ATCC 12633"
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Best Local Similarity 54.5%;
Matches 158; Conservative
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US-08-484-274-6

Perfect score:

Sequence:

Scoring table:

Searched:

Database :

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Glyphosate oxidore
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                   480022 seqs, 187831343 residues
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Listing first 45 summaries
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Query Match Length

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                                                                                        The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme which has been manipulated such that it is suitable for introduction into and expression in plant transformation vectors, but it still encodes the wild type GOR enzyme. It was obtd. from bacterial isolate LBAA. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops. See also Q20832-Q20841 and Q22705.
                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTTCTTGACCCGATGGGGCCGTTGTCA 240
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                                                                                                                                                                                                                                                                                                                                                                               Length 1321;
Gene encoding glyphosate oxido-reductase enzyme - used to
transform plants to produce plants tolerant to glyphosate
herbicide
                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                    Sequence 1321 BP; 292 A; 373 C; 369 G; 287 T; 0 other;
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                                                            Claim 1; Fig 3; 142pp; English.
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                  gcgacacctatggaaatggggcttcgcgtggcgggtacggttgagttcgctgggctcaca
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                                                                                                       GCGACACCTATGGAAATGGGGGTTCGCGTGGCGGGTACGGTTCGACTGGGGCTCACA
                                                                                                                                                                                          1081 ATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAACCCGGACACCCGACGTAATCTATGCT
                                                                                                                                                                                                                                                                                                                  CICCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGT
                                                                                                                  oxidoreductase coding region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "not present in alternative sequence"
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/note= "not present in alternative
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/note= "glyphosate
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                                                                                                               gtatctgcgcgtgtcatcggctttgagactgaaggtagggcgcttaaaggcattacaacc
                                                                                                                                          ACGAACGCCGTTCTGGCCGTTGATGCAGCGGTTGTCGCAGCCGGCGCACACTCGAAATCA
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transform plants to produce plants tolerant to glyphosate
herbicide
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Best Local Similarity 99.6%;
Matches 1291; Conservative
 91US-0717370
90US-0543236
                                                                   Kishore GM, Barry GF;
                                                                                             WPI; 1992-041559/05
                                         (MONS ) MONSANTO CO
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24-JUN-1991;
25-JUN-1990;
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                                                                CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCAGCGCCCGATGCGTTGCGGGATTTCGAT
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            present here'
                                            here'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1689;
                                                                                                                                                                                                                               Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide
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/*tag= c
/note= "in the alternative sequence '/*tag= d
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/note= "in the alternative sequence |
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Pred. No. 0;
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99.48;
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Best Local Simi
Matches 1288;
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25-JUN-1990;
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It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant.

Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops.
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7.tag= a
/note= "encodes wild type glyphosate oxidoreductase"
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                                                                                                                                                                                                                                                         Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.6%; Score 1200; 95.4%; Pred. No. 0;
                                                                                                                                                                                                                                                                                                         Claim 1; Page 102; 142pp; English.
 GOR; resistance;
                                                                                                                                                       91US-0717370
90US-0543236
                                                                                                                                      91WO-US04514
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Matches 1236; Conservative
                    Bacterial isolate LBAA.
                                                                                                                                                                                                           Kishore GM, Barry GF;
                                                                                                                                                                                      (MONS ) MONSANTO CO.
                                                                                                                                                                                                                               WPI; 1992-041559/05.
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 Recombinant;
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AGACCAAACAAGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
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                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme, the gene sequence was synthesised so that it could be redesigned to eliminate as much as possible the following sequences or redesigned to eliminate as much as possible the following sequences or restriction sites, while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more; A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + C% for the synthetic gene is 51% and the potential to form short, high energy, hair-pin structures is reduced. However it still encodes the wild type GOR enzyme. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tollerance of the plant.

Transformed plants realistant to glyphosate can be obtd, so that weeks a controlled in fields contg. crops.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 961.6; DB 13; Length 1296;
Pred. No. 3.7e-297;
0; Mismatches 209; Indels 0;
                                                                                                                                                                                                                                                                                                                         Gene encoding glyphosate oxido-reductase enzyme - used to
transform plants to produce plants tolerant to glyphosate
herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1296 BP; 271 A; 359 C; 305 G; 361 T; 0 other;
                                                             Synthetic glyphosate oxidoreductase gene.
                                                                                                                        Location/Qualifiers
1..1296
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1032; 142pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           also Q20832-Q20841 and Q22705
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 ВР
                                                                                Recombinant; GOR; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.2%;
ilarity 83.9%;
Conservative
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 DNA; 1296
                                        (first entry)
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                                                                                                                                                                                                                                                                                Kishore GM, Barry GF;
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020835 standard;
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Best Local Simi
Matches 1087;
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25-JUN-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
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                                                                                                                                                                                                            plant;
herbicide;
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Pred. No. 9.5e-297;
0; Mismatches 209; Indels 0;
                                                                                                                                                                                                      Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plan 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herb tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glyphosate resistant transgenic sugar beet plants
Sugar beet T-DNA containing cp4/epsps #2
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NOVARTIS-ERFINDUNGEN VERW GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tenning PP;
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83.98;
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Matches 1087; Conservative
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                                                                                       X57309 standard;
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A chemically inducible plant gene expression cassette which comprises an inducible promoter linked to a gene (I) that confers resistance to a herbicide, is claimed. (I) imparts resistance to N-phosphonomethylegivene (glyphosate) or its salts, but may also be a gene for resistance to, e.g. chhoroacetanilides, glufosinate, sulphonyl ureas, imidazolones, etc. The inducible promoter (e.g. alcA, alcA, alcA, aldA or other alcR-induced gene promoter) is operatively linked to an alcR regulator sequence. Induced expression of (I) avoids the risk that constitutive expression may interfere with plant development; allows volunteer plants to be controlled by herbicide applied without inducer and minimises the chance that herbicide-resistant strains of weeds will arise. The expression cassette is strictly controlled and suitable for general use in plants (both mono- and discyledons). The alcAlcR gene switch was exemplified with genes conferring resistance to glyphosate. The switch was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drive inducible expression of glyphosate oxidase (GOX) in plants. Switchable GOX was expressed alone or in conjunction with constitutive expression of 5-enol-pyruvylshikimate 3-phosphate (RPSPS) CP4. Constructs were optimised for expression in mono- and dicotyledonous crop species. The present sequence comprises a fusion of the GOX gene fused to the chloroplast transit sequence I from Arabidopsis RUBISCO (CPTI). This sequence was ligated into pWJBI (see TBS666) and used in construction of
                                                                                                                                                                    expression cassette: inducible promoter; alcA; alcA; regulator; alcohol dehydrogenase; herbicide resistance gene; glyphosate; herbicide resistance gene; glyphosate; herbicide resistance gene; glyphosate; GOX; EPSPS; 5-enol-pyruvylshikimate 3-phosphate CP4; chloroplast transit sequence 1; Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chemically inducible cassette for expressing herbicide resistance gene in plants - and derived plants, partic. for resistance to glyphosate, avoids constitutive expression and minimises development of herbicide tolerant weeds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96WO-GB01883
DNA; 1631
                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                        Chimeric Arabidopsis
                                                                                                                               CPT1-GOX gene fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-154273/14.
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T85664 standard;
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                                                                                    21-NOV-1997
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                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                      50; Gaps
 Length 1631;
                       Indels
  DB 18;
                       Mismatches 217;
Score 878.8; DB 18
Pred. No. 1.2e-270;
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 67.8%;
80.2%;
                       Conservative
           Similarity
                     Matches 1079;
  Query Match
Best Local &
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CGCTCCCCGTGATTGGCCGGGCAACCCGGACACCCGACGTAATCTATGCTTTCGGCCACG 1150 togigoticteaagggiatecaccaccaccaacggigitetigetgitgatgeigeagigit 1053 ccettggtgatgacatcccattggataccgaacgtggataccacatcgtgatcgccaacc 1173 790 910 335 395 455 515 575 933 695 993 453 693 753 873 ACTGGAAACGTGCGCATGTGCTCTATACGCACGCTCGAAAACTTCTTCCAGCCCTCGCGC tagecacettatecgteaeggteaecttacegtgtacegtggagaageagaettege TATAGAAGAAGGTCACACGATTAATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCG CGGAAGCCGCTCCACCATTCCGACGACCGATGCGTCAGGAAAATTCATCGCGACACCTA TGGAAATGGGGGTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACAGCCGCTCCTA tggagatgggtcttcgtgttgctggaaccgttgagttcgctggtctcactgctgctccta GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC -----CGATGGGGCCGTTGTCAATCCGGTTCAGCTATTTTCCAACCATCATGCCCTG GTTGATTCGCTTTCTGTTAGCCGGAAGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACT CCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGC GAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCGTGGAGAAGCAGACTTCGC CGCCGATGCGTTGCGGGATTTCGATCCGAACTTGTCGCATGCGTTTACCAAGGGCATTCT TAGGGCGCTTAAAGGCATTACAACCACGAAGGCGTTCTGGCCGTTGATGCAGCG----------GTTGTCGCACCGCCGCACACTCGCAATTCACTTGCTAATT CGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTCATCGCGAATC ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACC-1174 1234 1294 1354 1091 121 394 181 454 224 514 276 336 634 396 594 456 754 516 919 874 989 934 994 751 791 851 911 971 1031 g qq ò q 9 q q δ a ò g ò q q ò Q οy g δ q ò ò ò ò à ò ò ò d οy ò

¹ ATGGCTGAGAACCACAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG 60

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GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC
                                       gaaggtgcttctttcggtaacgctggttgcttcaacggttcctccgttgttccaatgtcc
                                                                           AGACCAAACAAGGTGAAGGAGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
                                                                                                                                                                                                                CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT
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                                                               ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGGGCCCTTGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvjshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
                                                                                                                                                                                                                                                                                                                  plant;
herbicide;
                                     ccttccagtgattggtcgtgctacccgtactccagacgttatctacgctttcggtcacg
                        GTCATCTCGGCATGACAGGGGCGCCGATGACCGCAACGCTCGTCTCAGAGCTCCTCGCAG
                                                                       GCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGTATTGGCAAAT
                                                                                                                                                                                                                                                                                                             Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plar
5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herk
tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 8798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glyphosate resistant transgenic sugar beet plants
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83.2%; Pred. No. 1.5e-204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                                                                                                                       Sugar beet T-DNA containing cp4/epsps.
                                                                                                                         CCAAGCAAACGGGTCCGGCAAGTTAA 1296
                                                                                                                                     Tenning PP;
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                                                                                                                                                                                                               ВP
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                                                                                                                                                                                                                                                               (first entry)
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Matches 766; Conservative
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                                                                                                                                                                                                              X57308 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                        WO9923232-A1
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herbicide;
                                                                7805 aacccacaaggtctcgtgactctcttgtttcgtcgtttcatcgctaacggtggagagttc
                                                                                                                                                                                                        cttgctaactcccttggtgatgacatcccattggataccgaacgtggataccacatcgtg
                                                  AATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCGTTTTTATCGCGAACGGTGGCGAATTT
                                                                                                                  GTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGGCCCTTAAAAGGCATTACAACC
                                                                                                                                                                                      ACGAACGGCGTTCTGGCCGTTGATGCAGCGGTTGTCGCAGCCGGCGCACACTCGAAATCA
                                                                                                                                                                                                                                                                                                                            841 ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACGATGCGTCAGGAAAATTCATC
                                                                                                                                                                                                                                                          CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sugar beet, transformation, T-DNA, insertion, cp4/epsps; plan
5-enolpyruvylshikimate-3-phosphate synthase, transgenic, herb
tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sugar beet T-DNA containing cp4/epsps fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X57305 standard;
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Gaps

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0; Mismatches 155; Indels

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7205 atggctgagaaccacaagaaggttggtatcgctggagctggaatcgttggtgtttgcact 7264

1 ATGCCTGAGAACCACAAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACG 60

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72.1 ACGAACGCCGTTCTGCCCGTTGATGCAGCGGTTGTCGCAGCCGGCGCACACTCGAAATCA 780
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                                               AATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCGTTTTATCGCGGAACGGTGGCGAATTT
                                                                                                              661. GTATCTGCGCGTGTCATCGCCTTTGAGACTGAAGGTAGGGCGCTTAAAAGGCATTACAACC
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/note= "homologous to the BioA gene"
424056..425594
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/note= "homologous to the OppD gene"
419677..420738
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/note= "homologous to the OppF ge
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/note= "homologous to the OppC ge
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/note= "homologous to the CapA
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complement (426949..428028)
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417796..418671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium species plasmid pNGR234a.
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V30458/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGGGCCGTTGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20; Length 8012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                           Glyphosate resistant transgenic sugar beet plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 51.8%; Score 671.4; DB 20;
Best Local Similarity 84.3%; Pred. No. 4.7e-204;
Matches 756; Conservative 0; Mismatches 141;
                                                                                                                                           (NOVS ) NOVARTIS AG.
(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                                              PP;
                                                                                                                                                                                                                                                                                            Claim 8; Page 24-29; 55pp; English.
                                                                                                                                                                                              Tenning
                                                                            98WO-EP06859
                                                                                                           97US-0112003
                                                                                                                                                                                            Steen P,
                                                                                                                                                                                                                           WPI; 1999-313347/26
                                                                                                                                                                                            Mannerloef M,
           WO9923232-A1
                                                                          29-0CT-1998;
                                                                                                           31-OCT-1997;
                                            14-MAY-1999
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/product= "ferrodoxin-like protein" /note= "homologous to the Nifo gene" 445088446602 /*tag= " /stag= "dctA" /product= "c4-dicarboxylate transport protein" /note= "homologous to the DctAI gene" /*tag= " /*tag	/47844 . 448500 /*tag= v / 448500 /*tag= v / 448500 /*tag= v / 5tandard_nanne= "ORF L2" /product= "gamma-hexachlorocyclohexane-dechlorinase-like /note= "homologous to the LinA gene" /#48497 . 450203 /*tag= v / 450203	/product=_numme=_onr_bs /product=_numme=_onr_bs /frag=_aa /standard_name=_"ORF_L4" /product=_nuciferase alpha-subunit-like protein" /note=_homologous to the LuxA gene" /*tag=_ab /standard_name=_"ORF_L6"	/gene= "nifp" /product="alpha-subunit of FeMo protein of nitrogenase" 454590. 456131 /*tag= ac /standard_name= "ORF L7" /gene= "nifk" /product= "beta-subunit of FeMo protein of nitrogenase" /*tag= ad	/standard_name= "ORF L8" /product= protein involved in FeMo co-factor blosynthesis" /note= "homologous to the NifB gene" 457687.,459096 /*tag= ae /standard_name= "ORF L9" /product= protein involved in FeMo co-factor blosynthesis" /note= "homologous to the FixF gene"	459093459575 /*tag= "A spiral to the spir	/*tag= ah /stadard_name= "ORF L12" /product= "protein similar to part of the Fe protein /product= "homologous to the NifiH gene" /fli28461345 /*tag= ah /standard_name= "ORF L13" /product= "protein of unknown function" /standard_name= "ORF L13" /product= "protein of unknown function" /standard_name= "ORF L14" /product= "peptidase-like protein"
CDS	CDS	CDS	cos	CDS	SOS CDS	CDS CDS
/product= "transposase homologue" /note= "homologous to the Tnp gene" 428292429623 /*tag= h /standard_name= "ORF K8" /product= "glutamate dehydrogenase-like protein" /note= "homologous to the GLUD1 gene" /complement (430538431284) /*tag= i /standard_name= "ORF K9" /product= "transposase homologue" /product= "transposase homologue" /*tag= i	/standard_name= "ORF K10" /product= "transposase homologue" /note= "homologous to the Tnp gene" complement (433880434110) /*tag= k /standard_name= "ORF K11" /product= "protein of unknown function" /note= "homologous to the FixU gene" /note= "homologous to the FixU gene"	/*tdg	/*tag* n /*tag* n /*tag* n /*tag* n /*tag* n /*tag* n /stadard_name= "ORF K14" /gene= "nifB" /product= "protein involved in FeMo co-factor blosynthesis" complement (436460438130) /*tag= o /standard_name= "ORF K15" /qene= "nifA"	/product= "positive regulator of nif, fix and other genes" complement (438297438590) /*tag= p /standard_name= "ORF K16" /gene= "fixx" /product= "product required for nitrogenase activity" complement (438605439912) /*tag= q /standard_name= "ORF K17"	/gene= Tixc. /groduct= "protein required for nitrogenase activity" /product= "protein required for nitrogenase activity" /*tag= r /standard_name= "ORF K18" /gene= "fixB" /product= "protein required for nitrogenase activity" /standard_name= "ORF K19" /*tandard_name= "ORF K19"	/gene="fixa" /gene="fixa" /product="protein required for nitrogenase activity" /product="protein required for nitrogenase activity" complement (442316442636) /*tag= t /standard_name="ORF K20 /rtag= u /*tag= u
S CD CDS	CDS	cos cos	CDS	SOD	CDS	CDS CDS
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Homo sapiens
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28-AUG-1998;
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                                                                                                                                             Db 395408 CTATTGGTCGCGTCTGCGCCCAATGACGCCGGGCGCGCCGTCGTCGTCGCCC---CAAC 395352
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                                                                                                                                                                           1056 CAAATGGATGGGGTTCCGGCCGAGCATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAAC 1115
                                                                                                                                                                                                                                                                    1176 GATGACCGCAACGCTCGTCTCAGAGCTCCTCGCAGCCGAAAAGACCTCAATCGACATTTC 1235
                                                                                                                                ACGCACGCTCGAAAACTTCTTC-CAGCCCTCGCGCCTGCGAGTTCTGAAGAACGATATTC 1055
                                                                                                                                                                                                                       1116 CCGGACACCCGACGTAATCTATGCTTTCGGCCACGGTCATCTCGGCATGACAGGGGCGCC 1175
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Symbiosis; open reading frame; ORF; plasmid; vector; transportation; degradation; metabolism; host range; nitrogen fixation; nodulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the nucleotide sequence of the plasmid pNGR234a isolated fro
Rhizobium sp. NGR234. Open reading frames (ORF) derivable from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 - used to
                                                                                                                                                                                                                                     Db 395351 GAAGATCGCCGGTCTCTTAACACCGGGCACGCACGCTTGGCTGGACGACGATGAGCTC
                                                                                                             4
                                                                                       Length 534720;
                               /standard_name= "ORF L15"
/product= "processing protease-like protein"
/note= "homologous to the PP gene"
466590..467021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated symbiotic plasmid from Rhizobium sp. NGR234 - develop products for modifying plant characteristics, e.g. fixation, synthesis of compounds and stress response
                                                                                                             Indels
 /note= "homologous to the bI-MPP gene"
464736..466079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenthal A;
                                                                                                          0; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAB BIOLOGIE MOLECULAIRE PLANTES SUPERIE
                                                                                     Score 37; DB 19;
Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhizobium species symbiotic plasmid pNGR234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perret XP,
                                                                                                                                                                                                                                                                                                                            Db 395231 CGACCTCGCCGTCAGCCGCTACGCT 395207
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                                                                                                                                                                                                                                                                                                               1236 GCCCTTCGCACCAAACCGCTTTGGT 1260
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                                                                                                                                                                                                                                                                                                                                                                                          V30459 standard; DNA; 536165
                                                                                     2.9%;
llarity 51.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Broughton WJ, Freiberg CB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                       /*tag=
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                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       legume; plant; ds
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                                                                                                          Matches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUL-1999
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                                                                                       Query Match
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V30459/c
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nucleotide sequence are claimed. The nucleotide sequences or ORFs can be used e.g. in the transportation of compounds to and from an organism which is a host to at least one of the nucleotide sequences, ORFs or proteins, the degradation and/or metabolism of organic, inorganic, natural or xenoblotic substances in a host organism or the modification of the host range, introgen fixation abilities; for obtaining a synthetic especially for nodulation efficiency on host plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 395468 ACGCACACTCGAGCATTCCGTCATGGACCTCTTTCCCGGGGGGATGCAAAAGAAGATC 395409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              395291 CGGCTCTGCCCGCGTCATTGGGAGCCGGGAGCCCGAGATCGACGCCAC 395232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          997 ACGCACGCTCGAAAACTTCTTC-CAGCCCTCGCGCCTGCGAGTTCTGAAGAACGATATTC 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease; angiogenesis; inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder; diabetic retinopathy; macula degeneration; haemangloma; detection; arterial-venous malformation; immune deficiency; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                Sequence 536165 BP; 111291 A; 155755 C; 157864 G; 111255 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1056 CAAATGGATGGGGTTCCGGCCGAGCATCCCGGATTCGCTCCCCGTGATTGGCCGGGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1116 CCGGACACCCGACGTAATCTATGCTTTCGGCCACGGTCATCTCGGCATGACAGGGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1176 GATGACCGCAACGCTCGTCGAGGCTCCTCGCAGGCGAAAAGACCTCAATCGACATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4
                                                                                                                                                                                                                                                                                                                                                                                              Length 536165;
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Pred. No. 1.8;
0; Mismatches 125; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395231 CGACCTCGCCGTCAGCCGCTACGCT 395207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1236 GCCCTTCGCACCAAACCGCTTTGGT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human METH1 related EST AL021529.
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                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.9%;
Best Local Similarity 51.3%;
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232020 standard; DNA; 38734
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98US-0098539
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(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-590684/50
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Tue Jan

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metalloprotease thrombospondin (METH) proteins METH1 and METH2
metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH12 have been found to be potent inhibitors of
anglogenesis both in vitro and in vivo. They can be used for treating
cancer and other disorders related to anglogenesis including abnormal
wound healing, inflammation, rheumatold arthritis, psoriasis,
endometrial bleeding disorders, diabetto retinopathy, some forms of
macula degeneration, haemanglomas, and arterial venous malformations.
They may be useful in treating deficiencies or disorders of the immune
system, by activating or inhibiting the proliferation, differentiation,
or mobilisation (chemotaxis) of immune cells. The etiology of these
immune deficiencies or disorders may be genetic, somatic, such as
cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or
toxins), or infectious. They can also be used to treat inflammatory
conditions, both chronic and acute conditions. The products can also be
used for detection and diagnosis. 232002 to 232080, and ¥49503 to ¥49511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38050 gcaacggcgtctgctccgaccgccaggagtcgctgtcgcgcacaccccagacggtgacgc 38109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38110 cgaggcagcggagacggccaggcagtcgttggtcacgttggcgtaggtcgaggccgggg 38169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCTTCAACGGCTCATCCGTCGTCCTATGTCCATGCCGGGAAACTTGACGAGCGTGCCGA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AGTGGCTCCTTGACCCGATGGGGCCGTTGTCAATCCGGTTCAGCTATTTTCCAACCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 TGCCCTGGTTGATTCGCTTTCTGTTAGCCGGAAGACCAAACAAGGTGAAGGAGCAGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      329 AAGCACTCCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGCGGAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 20; Length 38734;
Pred. No. 2.1;
0; Mismatches 135; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38734 BP; 6142 A; 13140 C; 13585 G; 5867 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of ORF33512 encoding a virulence factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection; ss.
                                                                             Disclosure; Page 296-321; 457pp; English
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Best Local Similarity 46.2%;
Matches 116; Conservative
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                                                                                                                                                                                                                          sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is appable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.

Is a P. aeruginosa infection. The specification were poorly legible, and in some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                               The present sequence represents a Pseudomonas aeruginosa nucleic aicd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 CGCCGCGGATTCAAAGTCACCTTGATTGACCCGAACCTTCTGGCGAAGGTGCATCGTTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 AAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACGGCGCTGATGCTTCAG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mahajan-Miklos S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of ORF33205 encoding a virulence factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human pathogen; virulence polypeptide; virulence factor; pathogenic infection; Pseudomonas aeruginosa infection; ss.
                                                                                                                                                  Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 405 BP; 98 A; 135 C; 97 G; 75 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 2.6%; Score 34; DB 20;
Best Local Similarity 52.9%; Pred. No. 0.44;
Matches 73; Conservative 0; Mismatches 65.
                                                                          Goodman HM,
                                                                                                                                                                                  Disclosure; Fig 4; 228pp; English.
                                                                        ς, υ,
                                                                        Drenkard
Tsongalis
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                                         (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 GCGGGAGGCGGGATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                   WPI; 1999-357851/30.
                                                                      Ausubel F, Cao H,
Rahme LG, Tan M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X98167 standard;
            25-NOV-1997;
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sequences from microorganisms - without the need

novel DNA

Sandal T;

Kauppinen S,

Diderichsen B,

us-08-484-274-6.rng

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Search completed: January 1, 2001, 03:42:34 Job time: 20162 sec
                                                                                         for culturing the microorganism
                                      WPI; 1998-008878/01
                                                     P-PSDB; W44270
               Dalboge H,
                                                                            Solating
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                                                                                                             The present sequence represents a Pseudomonas aeruginosa nucleic aicd sequence. P. aeruginosa is an opportunistic human pathogen present in soil water and plants. The specification describes virulence polypeptides and nucleic acid sequence encoding such polypeptides. These sequences can be used to identify a compound which is capable of decreasing the expression of a pathogenic virulence factor. Compounds that inhibit the expression or activity of virulence factor polypeptides can be used to treat pathogenic infections, especially where the infection is a P. aeruginosa infection.

Is a P. aeruginosa infection.

In some instances assumptions were made as to the identity of the base; it is therefore possible that the sequence given below is not entirely
                                                                                                                                                                                                                                                                                                                                                                                                                                  76 CGCCGCGGATTCAAAGTCACCTTGATTGACCCGAACCCTCCTGGCGAAGGTGCATCGTTT 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                  393 CTCGCCGGACTGCGGGTGACCCTGGTGGACGCGCGAGAGTGGGCCGTGAGGCATCCTGG 334
                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                          453 AGAGATGTAGTAGTGGTAGGCGCTGGCGTCATCGGCCTGTTGACCGCCCGGGAGCTGGCG 394
                                                                                                                                                                                                                                                                                                                                                                                 16 AAAAAAGTAGGCATCGCTGGAGCCGGAATCGTCGGCGTATGCACGGCGCTGATGCTTCAG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            core region; isolation; microorganism; identification;
  ŝ
  Mahajan-Miklos
                                                                                                                                                                                                                                                                                                                                  DB 20; Length 603;
                                                             Virulence factors useful in developing disease treatments
                                                                                                                                                                                                                                                                                                                                                          65; Indels
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                                                                                                                                                                                                                                                                                            Sequence 603 BP; 119 A; 219 C; 171 G; 94 T; 0 other;
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/*tag= a
/product= "hybrid gene construct"
 Goodman HM,
                                                                                                                                                                                                                                                                                                                                  Score 34; DB 2
Pred. No. 0.54;
0; Mismatches
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                                                                                      Disclosure; Fig 3; 228pp; English
Drenkard E,
Tsongalis J;
                                                                                                                                                                                                                                                                                                                                  2.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V15073/c
ID V15073 standard; DNA; 922 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 GGGAATGCCGGATGCTTC 153
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                                                                                                                                                                                                                                                                                                                                                          Conservative
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/*tag=
                                    WPI; 1999-357851/30.
 Cao H,
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 73; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hybrid DNA; ss
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              Rahme LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cellulase
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The present sequence represents a novel hybrid gene construct from an example of the present invention. The present invention describes a novel method for providing a novel DNA sequence encoding a polypeptide from a microorganism with an activity of interest. The method comprises: (i) PCR amplification of the DNA with PCR primers with homology to (a) known gene(s) encoding a polypeptide with an activity of interest; (ii) linking the obtained PCR product of a 5' structural gene sequence and a 3' structural gene sequence; (iii) expressing the resulting hybrid DNA sequence; (iv) screening for hybrid DNA sequences nociding a polypeptide with the activity of interest or a related activity; and (v) isolating the hybrid DNA sequence identified in step (iv). This method provides for identification and isolation of sequences from microorganisms without having to cultivate and isolate the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGCGTTTACCAAGGGCATTCTTATAGAAGAACGGTCACACGATTAATCCGCAAGGG 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 CCACGGGGAGTTGTTGCTGCAGGTGTAGGAAGTGCCGCCGTTGCAACCGCTCACGGCGTT 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           613 CTCGTGACCCTCTTGTTTCGGCGTTTTATCGCGAACGGTGGCGAATTTGTATCTGCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 CTCGGAGCCTCCAGAGAGCTTGGTAGCGGCAAAGCCATAGGCGAGGTTGTCGTTGACAGC
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Pred. No. 0.67;
0; Mismatches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 GGCGTCGGAGATGGGGTTGTCGTTCTTGTCGCAGGTCA 156
Example 3; Page 53-54; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 2.6%;
al Similarity 47.2%;
103); Conservative
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Best Local 9
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Sequence 5, Appliance 20, Appliance 1, Appliance 17, Appliance 19, Appliance 19, Appliance 104, Appliance 1, Appliance 2, Appliance 1, Appliance 1, Appliance 2, 
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1, Appli
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                           US-08-314-309A-5
US-08-314-309A-2
US-08-314-309A-3
US-08-14-759-17
US-09-144-759-19
US-09-144-759-21
US-08-469-537A-104
US-08-469-986-1
US-08-462-484-3
US-08-461-147-3
US-08-441-147-3
US-08-441-3
US-08-441-147-3
US-08-441-3
US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISH PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-440-845D-8
US-08-391-339-7
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Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
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FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/07/717,370
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REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHRACTERISTICS:
LENGTH: 1296 base pairs
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100.0%;
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423
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Best Local Similarity
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                                                                                                                                                                                                                     Search time 157.96 Seconds (without alignments) 1240.873 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGCCTGAGAACCACAAAAA.........AAACGGGTCCGGCAAGTTAA 1296
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Sequence 6,
Sequence 3,
Sequence 4,
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/6_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESSEDNOBENCE ADDRESS:
ADDRESSE: Arnold, White & Durkee
                                                                                                                                                                                                                               1261 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ...oreSSEE: Arnold, White & Durkee STREET: P.O. Box 4433
CTTY: Houston STATE: Texas COUNTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08484274A Patent No. 5776760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PALLELSON, Mellinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT:
TELECOMMUNICATION INFORMATION:
TELECHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 6:
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Matches 1296; Conservative
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STRANDEDNESS: double
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                                         ATCCGGTTCAGCTATTTCCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGA 300
                                                AGACCAAACAAGGTGAAGGAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
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                    AATCCGCAAGGCCTCGTGACCCTCTTGTTTCGGCGTTTTTATCGCGAACGGTGGCGAATTT
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                                                                                                                                                              APPLICANT: Kishore, Ganesh M.
APPLICANT: Rishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TILE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
                                     1261 ATTGCCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
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Pred. No. 0;
0; Mismatches
ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA
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CARSEICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATTERSON, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBILIS
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1692 base pairs
                                                                                                                                 US/08484274A
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Best Local Similarity 99.6
Matches 1293; Conservative
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                                                                                                                                 Sequence 3, Application
Patent No. 5776760
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                                                                                          RESULT 3
US-08-484-274A-3
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Tolerant Plants

Gl.yphosate 33

NUMBER OF SEQUENCES: 3.
CORRESPONDENCE ADDRESS:

Gerard

APPLICANT: Barry, G TITLE OF INVENTION:

ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway

ADDRESSEE: Monsar STREET: 700 Chest CITY: St. Louis STATE: Missouri

USA

COUNTRY:

63198

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NAME: HOETNER, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 4:
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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

OPERATING SYSTEM: SOFTWARE: PatentI

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible

APPLICATION NUMBER: US/08/391,339

FILING DATE: CLASSIFICATION: 800

PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/156,968 FILING DATE:
APPLICATION NUMBER: US/07/717,370

ATTORNEY/AGENT INFORMATION: NAME: Hoerner, Dennis R.

FILING DATE:

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                                                                                                                                            DB 1;
                                                                                                                                         96.9%; Score 1255.2;
99.5%; Pred. No. 0;
ive 0; Mismatches
                                                          MOLECULE TYPE: DNA (genomic)
SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
TYPE: nucleic acid
                                                                                                                                                              Matches 1290; Conservative
                                       double
                                                  Linear
                                                                                                                                                     Similarity
                                   STRANDEDNESS:
                                                                                 NAME/KEY:
LOCATION:
                                                  TOPOLOGY:
                                                                                                       US-08-391-339-4
                                                                                                                                          Query Match
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Sequence 4, Application US/08391339 Patent No. 5463175 GENERAL INFORMATION: APPLICANT: Kishore, Ganesh M.

US-08-391-339-4

Ganesh M.

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AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG 360
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                                                                                               MEDIUM TYPE: Chippy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE SOFTWAND
SOFTWARE: Patentin PC-Dos/Ms-Dos
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMM: PATENTON NUMBER: 33,062
REFERENCE/DOCKET NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBTI30 38-21(13560)A
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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llarity 99.5%; Pred. No. 0;
Conservative 0; Mismatches
             White &
                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                             LENGTH: 1293 base pairs
            ADDRESSEE: Arnold, Wh. STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
  CORRESPONDENCE ADDRESS:
                                                                          ZIP: 77210-4433
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 1290; Conserv
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                                                               COUNTRY:
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
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                    CCGAACTTGTCGCATGCGTTTACCAAGGGCATTCTTATAGAAGAAGAACGGTCACACGATT
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ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08391339 Patent No. 5463175 GENERAL INFORMATION:
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ZIP: 631
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                                         PatentIn Release #1.0, Version #1.25
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99.5%; Pred. No. 0;
1ve 0; Mismatches
                                                                                                                                                                                                                                     38-21(10533)
                                                                   APPLICATION NUMBER: US/08/391,339 FILING DATE: USASIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/156,968
                                                                                                                                              FILING DATE:
APPLICATION NUMBER: US/07/717,370
         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                       NAME: Hoerner, Dennis R., Jr. REGISTRATION UNBER: 30,514
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   TELEPHONE: (314)537-6099 INFORMATION FOR SEQ ID NO: 3
Floppy disk
                                                                                                                                                                                                                                                                                                              LENGTH: 1689 base pairs
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Best Local Similarity
Matches 1290; Conserv
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                                                                                                                                                                                                                                                                                                                             TYPE:
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Query Match 92.7%;
Best Local Similarity 95.4%;
Matches 1237; Conservative
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                 AATCCGCAAGGGCTCGTGACCCTCTTCTTTCGGCGTTTTTATCGCGAACGGTGGCGAATTC
                                    CTATCTGCGCGTGTCATCGGCTTTGAGACTGAAGGTAGGGCGCTTAAAAGGCATTACAACC
                                                                          ACGAACGCCGTTCTCCCCGTTGATGCAGCGGTTGTCGCAGCCGGGCGCACACTCGAAATCA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08391339 Patent No. 5463175 GENERAL INFORMATION:
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US-08-391-339-7
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FILING DATE:
CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/717,370
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
FILECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
FILECOMMULICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: MOLECULE TYPE: DNA (recombinant)
US-08-391-339-7
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Pred. No. 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tole
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Patterson, Melinda L. REGIESTRATION NUMBER: 33,062 REFERENCE/DOCKET NUMBER: MOI TELECOMMUNICATION INFORMATION:
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1: 435
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                                                                                                                                                                                           Pred. No. 0;
0; Mismatches
                                                                                                                                                                            Score 1201.6;
                          SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                            92.7%;
TELEPHONE: (713)789-2679 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                          Best Local Similarity 95.4
Matches 1237; Conservative
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TOPOLOGY:
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                    GCGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                  1261 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30,914
ER: 38-21(10533)
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APPLICATION NUMBER: US/08/391,33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: HOGENER, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(1)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEO ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                      US-08-391-339-8; Sequence 8, Application US/08391339; Patent No. 5463175
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COMPUTER READABLE FORM:
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PRIOR APPLICATION DATA:
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STRANDEDNESS:
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                                                           Length 1296;
                                                                                       Indels
                                                                                    0; Mismatches 209;
                                                           DB 1;
                                                           Score 961.6;
Pred. No. 0;
; MOLECULE TYPE: DNA (synthetic) US-08-391-339-8
                                                         Query Match 74.2%;
Best Local Similarity 83.9%;
Matches 1087; Conservative
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBTI30 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Pred. No. 0;
0; Mismatches 209;
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                                                                                                                                                                                                                                                                             Sequence 8, Application US/08484274A Patent No. 5776760
                                                                                                                                                                                                                                                                                                        APPLICANT: Klahore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (synthetic)
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Best Local Similarity 83.9
Matches 1087; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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TOPOLOGY: linear
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ZIP: 77210-4433
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CITY: Houston
STATE: Texas
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                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                       ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
                                                                                                                                                                                                                                                                                                700 Chesterfield Village Parkway
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83.7%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: HOERNEY, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
FILING DATE:
                                                                                                                                                                                                                                                                         ADDRESSEE: Dennis R. Hoerner, Jr., ADDRESSEE: Monsanto Co. BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
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                                                                                                                                                               US-08-391-339-17
; Sequence 17, Application US/08391339
; Patent No. 5463175
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INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
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STATE: Missouri
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Matches 1085; Conserv
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US-08-391-339-17
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                                                                                                                                                                                                                                                   ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERNEZ/DOCKET NUMBER: MOBIL30 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 958.4; DB 2;
Pred. No. 0;
0; Mismatches 211;
                                                                                                             Sequence 17, Application US/08484274A
Patent No. 5776760
GENERAL INFORMATION: ALSHORE, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                    1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                          ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/484,274A FILING DATE: 07 June 1996 CLASSIFICATION: 435
                                                                                                                                                                                                  ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ 1D NO: 17: SEQUENCE CHARACTERISTICS: LENGTH: 1296 base pairs TYPE: nucleic acid STRANDEDNESS: double
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83.78;
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Best Local Similarity 83.7'
Matches 1085; Conservative
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US-08-484-274A-17
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             AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCAAGTCCACGGTG
                                                                      361 CCTTTGATCAAGTCCTTGGCTGAGGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT
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4.3%; Score 56.2; DB 1; Length 69;
Best Local Similarity 88.4%; Pred. No. 1.3e-09;
Matches ,61; Conservative 0; Mismatches 8; Indels
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Patent No. 5776760

GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants;
NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:
ADDRESSEE: Arrold, White & Durkee
STREET: P.O. Box 4433

CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
                                                                                                    COMPUTER REGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38-21(10533)
                                                                                                                                                                                                                                                              FILING DATE:
CLASSIETCATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/717,370 FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA (synthetic)
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CLASSIFICATION: 435
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COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:
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                    St. Louis
: Missouri
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                                           STATE: M. COUNTRY:
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Patent No. 5463175
CENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants;
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
                                                       Sequence 30. Application US/08391339
Fatent No. 5463175
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
TILLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Hoerner, Dennis R., Jr.
REGISTRATHON NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 800
PELOR PELICATION DATA:
APPLICATION NUMBER: US/08/156,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 88.49
Matches 61; Conservative
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STRANDEDNESS: single
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CITY: 8t. Louis
STATE: Missouri
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Search completed: January 1, 2001, 03:17:58 Job time: 29302 sec

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           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summarles
                                                                  OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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em_gss16:*
                                                                 gb_gss24:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length Ç 000

AL307658 Tetraodon AW247455 WillOS pep AV190084 AV190084 C47876 C47876 Yuji AV386799 AV386799 AV316270 AV316770 AL387587 MtBC43807 AL160534 Leishmani AQ328054 nbxb00421 AL106058 Drosophil AW500960 UI-HF-BPO AW501280 UI-HF-BPO AV413471 AV413471 AV418403 AV418303 AV418904 LýVET12e AV47698 AV427698 AV408977 AV406977 AV40855 AV407852 AV40855 AV407853 AV40855 AV408636 AV40813123 AV415123 AV423367 AV423367 BE357122 DGL_146_B AW925090 WS1_75_CO BE357121 DGL_146_B BE357121 DGL_146_B BE357121 DGL_146_B AA871231 vq32902.r AA542047 vk43d01.r AQ447252 mgxb0006C AV536254 AV536254 AA644181 ab63a02.s AL097775 Drosophil B07704 318H1F05706 AL267874 Tetraodon AW097371 rs43a11.y BE248875 NF023D11D W09527 ma01b07.rl D40242 RICS2075A R AQ328054 1 CNS01280 AW501280 3 CNS04UDT AW24765 AV190084 C47876 C47876 AV316270 AV387587 AW39751 BE248875 AV427698 AV416837 AV412853 AV425451 AV407852 AV408636 AV415123 BE351122 AW925090 BE357121 CNS002K5 B07704 CNS0320P AV413471 AV418303 AW719954 W09527 D40242 AA871231 AA542047 AQ447252 AV536254 AA644181 O

ALIGNMENTS

RESULT P149R/c

C41677 C41677 Yuji AL245876 Tetraodon BE411304 ISCO04 BI BE356986 DGL_146_B AU088715 AU088715 BE517838 WHE0803_C

CNS03IPN

333.00 333.00 333.00 333.00 333.00 333.00

C41677

BE356986 AU088715 BE517838

Direct Submission
Submitted (14-MAR-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and alicat@sanger.ac.uk see http://www.ebi.ac.uk/parasites/leish.html
Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L_major/
The primer sequence can be obtained from allcat@sanger.ac.uk. Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnollophyta; Liliopsida; Poales; Poaceae; Oryza.

Mang, R.A. and Dean, R.A.

A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)

Contact: Wing RA

Clemson University Genomics Institute ö Ivens, A.C., Lewis, S.M., Bagherzadeh, A., Zhang, L., Chan, H.M. and Smith, D.F. P149R 434 bp DNA GSS 16-MAR-2000 Leishmania major Friedlin PAC P149 right end-sequence, genomic 94 ACCTTGATTGACCCGAACCCTCCTGGCGAAGGTGCATCGTTTGGGAATGCCGGATGCTTC 153 297 GTTCTTGTCGATCGCCCCCCCCCCCCCCACCCCCTATGCCAACGCGGCTTCATC 238 AQ328054 702 bp DNA GSS 08-JAN-1999 nbxb0042102f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0042102f, DNA sequence.
AQ328054.1 GI:4119904 34 GGAGCCGGAATCGTCGGCGTATGCACGGCGCTGATGCTTCAGCGCCGGGGATTCAAAGTC 93 2 (bases 1 to 41) Taylor,R.G., Huckle,E.E.J., Ivens,A.C., Rajandream,M.A. and Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; ö % Score 44.4; DB 124; Length 434; Local Similarity 54.2%; Pred. No. 0.022; los 90; Conservative 0; Mismatches 76; Indels 0; Swith D.F. Agnerzadeh, A., Zhang, L., Chan, A physical map of the Leishmania major Friedlin genome Genome Res. 8 (2), 135-145 (1998) 154 AACGGCTCATCCGTCGTCCTATGTCCATGCCGGGAAACTTGACGA 199 /organism-"Leishmania major" /strain-"Friedlin" /db_xref-"taxon:5664" /clone-"PAC P149" AL160534.1 GI:7258935 Leishmania. 1 (bases 1 to 434) Leishmania major. Leishmania major survey sequence. AL160534 Oryza sativa. Barrell, B.G. Query Match LOCUS DEFINITION source BASE COUNT ORIGIN LOCUS DEFINITION ORGANISM RESULT 2 AQ328054/c ORGANISM JOURNAL MEDLINE REFERENCE TITLE JOURNAL ACCESSION VERSION AUTHORS TITLE JOURNAL COMMENT Matches ACCESSION VERSION KEYWORDS SOURCE AUTHORS REFERENCE AUTHORS REFERENCE KEYWORDS SOURCE FEATURES TITLE COMMENT pp qq ò ö

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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC and Genevieve Payan. It has been constructed in the vector
  Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 380)
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CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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National Institutes of Health, Mammallan Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                              1. .922
/organism="Drosophila melanogaster"
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/clone="BACN15P08"
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32.2%; Pred. No. 4.8;
iive 45; Mismatches
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Best Local Similarity 32.2%
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                   /db_xref="taxon:452"
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/clone="nbxb0042102f"
/clone="lb="codi"
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/lab_bost="E. coli Dil10B"
/rote="vector: pBeloBAC11; Site_1: HindIII: Site_2:
/note="vector: pBeloBAC11; Site_1: HindIII: Site_2:
HindIII: Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n-24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
library contains 36, 864 clones with an average insert size
of 128.5 Kb providing 10.9 haploid genome equivalents. The
deep coverage allows the isolation a particular sequence
with a probability of 99.9 %. Two high density filters,
each containing 18,432 clones (doubly spotted), represent
the whole library for colony screening."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 GETCGAGGCGCGCGCTTACCCATCGAAGCCGCCTCGTCTCCCTGGAAATCGAAAAGCG 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         378 GCCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCG 437
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
       Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
class: BAC ends
High cm. 1
                                                                                                                                                                                                                                        /organism="Oryza sativa"
/strain="Japonica"
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/cell_line="MGC85"
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                                  1. .380
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/db_xref="taxon:9606"
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 466-1550
Email: Robert_Strausbergenth.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Standt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-blo.llnl.gov/bbrp/lange/limage.html
Seq primer: MI3 Forward.
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 389)
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/cell_type="germinal center B cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
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Seg primer: Ml3 Forward
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AW501280.1 GI:7114663
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Sost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                          /note="Vector: pT773-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (4.4-7.4kb). Directionally cloned Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
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Tetraodon nigroviridis genome survey sequence SP6 end of clone
027A06 of library B from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 CIGAICAAGICATIGGCGGAGGAGGCIGAIGCGAGCCAICIGAICCGCCAIGAAGGICAI 423
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                                                                                                                                                                                                                                                                                                                                               Score 36; DB 22; Length 389;
Pred. No. 6.7;
0; Mismatches 90; Indel®
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/db_xref="taxon:99883"
/clone="027A06"
/lab_host="DH10B (LTI)"
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Best Local Similarity 50.0%;
Matches 90; Conservative
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Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohara, Y., Shin-i, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H.,
Nishigaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and
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1 (bases 1 to 382)

1 (bases 1, Motolashi, T., Tabara, H., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A. and Nishigaki, A.
                                                        AV190084 360 bp mRNA EST 22-JUL-1999
AV190084 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk566f3 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C47876 382 bp mRNA EST 18-OCT-1999 C47876 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk453a5 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 GCCGATGACCGCAACGCTCGTCTCAGAGCTCCTCGCAGGCGAAAAGACCTCAATCGACAT 1232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                               Expressed genes in C.elegans
Unpublished (1999)
Contact: Yuli Kohara
Gene Library Lab
National Institute of Genetics
Yafa 1111, M.shima, Shizuoka 411, Japan
Tel: 81-559-81-6854
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53.2%; Pred. No. 13;
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="yk566f3"
/clone_lib="Yuji Kohara
hermaphrodite embryo"
/sex="hermaphrodite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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105 c 109 g
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Caenorhabditis elegans
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C47876.1 GI:2384129
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DEFINITION
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KEYWORDS
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                                                                              DEFINITION
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KEYWORDS
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                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I; Lamiales; Lamiaceae; Mentha.
1 (bases 1 to 614)
Lange, B.M., Wildung, M.R., Stauber, E.J., Sanchez, C., Pouchnik, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probing essential oil biosynthesis and secretion by functional evaluation of expressed sequence tags from mint glandular trichomes Proc. Natl. Acad. Sci. U.S.A. 97 (6), 2934-2939 (2000) Contact: Lange, B.M.
Institute of Biological Chemistry/Washington State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mentha x piperita
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
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ML105 peppermint glandular trichome Mentha x piperita cDNA, mRNA
sequence.
                                                                                                                                                       970 AACTGGAAACGTGCGCATGTGCTCTATACGCACGCTCGAAAACTTCTTCCAGCCCTCGCG 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 AAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTGCGGCGTCTCAACGGTGTTCGCA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         435 AATCGGAAATCCCCCAAGGGGGGAAGGCTTCCTTCAGANTCTTCTCGATGTTCTTCGAG 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375 ATCAGCCCGGCCACGTCCTTGAGGAGGTGGAAGGTGAGGCCCACCTCCCGGAGGTGGCCG 31.6
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                                                                                                                                                                                                                                  1030 CCTGCGAGTTCTGAAGAACGATATTCCAAATGGATGGGGTTCCGGCCGAGCATCCCGGA 1088
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                                                                            Length 895
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/tissue_type="peltate glandular trichomes"
/cel=_type="secretory"
/cel=_Yvetor: lamba ZAPII" 1 others
    others
                                                                                                                   53; Indels
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  25
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Pred. No. 9.8;
0; Mismatches 120;
                                                                            DB 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: lange-m@mail.wsu.edu.
Location/Qualifiers
1. 614
/organism="Mentha x piperita"
/cultivar="Black Mitcham"
/db_xref="taxon:34256"
                                                                                               8.2;
  ىد
                                                                                                                   0; Mismatches
  227
                                                                            Score 36;
Pred. No.
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Matches 107; Conservative
  216
                                                                                               Similarity
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Matches 107; Conservative
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                                                                           Query Match
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Kazusa DNA Research Institute
Yana 1532-3, Klsarazu, Chiba 292-0812, Japan
Emall: yankamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Asamizu, E., Nakamura, Y., Sato, S., Fukuzawa, H. and Tabata, S. A Large Scale Structural Analysis of cDNAs in a Unicellular Green Alga, Chlamydomonas reinhardtii. I. Generation of 3433 Non-redundant Expressed Sequence Tags
DNA Res. 6, 369-373 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_llb="Chiamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_l: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV386799 517 bp mRNA EST 21-JAN-2000 AV386799 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CM007a05_r, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1173 GCCGATGACCGCAACGCTCGTCTCAGAGCTCCTCGCAGGCGAAAAGACCTCAATCGACAT 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1113 AACCCGGACACCACGACGTAATCTATGCTTTCGGCCACGGTCATCTCGGCATGACAGGGGC 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 GACGCAGGTCTCCATCTGCGTCGAAGAGCCCCCCCCCCGCAGCGAAGAGACGCCCCTCACCAT 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                               /strain="N2"
/db_xref="taxon:6239"
/db_clone="yk45385"
/clone=lyk47vjj Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 382;
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                                                                                                                                                                                                /organism="Caenorhabditis elegans"
                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                                                                                             , DB 36;
, 13;
                                                   Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Expression map of the C.elegans genome Unpublished (1996)
Contact: Yuji Kohara
                                                                                                                                                                                                                                                                                                                                                                                                            Score 35; DB 3
Pred. No. 13;
0; Mismatches
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/clone="CM007a05_r"
                                                                                                                                           Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                     /sex-"hermaphrodite
                                                                                                                                                                                                                                                                                                                         /dev_stage="embryo"
112 c 116 g
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Chlamydomonas reinhardtii
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                                                                                                                                                                                                                                                                                                                                                                                                             2.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             74; Conservative
                                                                                                                                                                            1. .382
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          110
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TITLE
JOURNAL
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TITLE
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Konno, H., Alzawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukuda, S., Fukuda, T., Hara, A., Hayeleu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, K., Kaya, S., Kusakabe, M., Matsuyama, T., Mki, R., Mizuno, Y., Koya, S., Kusakabe, M., Matsuyama, T., Mki, R., Mizuno, Y., Nakmura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Salto, H., Saro, K., Shibata, K., Shibata, Y., Salto, H., Saro, K., Shibata, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Watanabe, S., Yamamura, T., Yasunishi, A., Watanabe, S., Yamamura, T., Yasunishi, A., Watanabe, M., Tominaga, N., Tsunoda, Y., Noshiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Watanabe, S., Yamamura, T., Yasunishi, A., Watanabe, S., Yamamura, T., Yasunishi, Y., Kota, Y., Kikin Mouse ESTS (Konno, H., et al. 1999)

L. Unpublished (1999)

Contact: Yoshihide Hayashizaki
Genome Exploration Research Group, Life Science Tsukuba Center, Genome Stlence Laboratory
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Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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URL:http://genome.rtc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
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                                                                                                                                                                                                                                                                                                                               321 GCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGC 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 GGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCGTGG 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 CGACGACGAGGAGGAGGAGGCCAAGTAAACGGCATCGTTGCCTACTCGCGGTACTTG 354
                                                                                                                                                                                                                                                                                                                                                                              235 CATGGGGACGAACGACCTTCCCGAGACCACGACGAGGAGGGTGACGACGATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          441 AGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTGCGGCGTCTCAACGGTGTTCG
                                                                                                                                                             Length 517;
                                                                                                                                                                                                   Pred. No. 14;
0; Mismatches 120; Indels
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Tel: +81-298-36-9013
Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501 CACGCAGATCCTCAGCGCCGATGCGTTGCGGGATTTCGATCCGAACT
                                                                                                                                                                 DB 18;
82
                                                                                                                                                                 Score 35;
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    185
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138 t
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                                                                                                                                                                                                             /cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBC43E07"
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Matches 6
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                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
/strain="C57BL/6J"
/clone="1830455F07"
/clone=11D="RIKEN full-length enriched, adult male thymus"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second
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Estaryota: Viridiplantae: Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Ist strand cDNA was GAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL387587 494 bp mRNA EST 03-AUG-2000
MLBC43E07F1 MtBC Medicago truncatula cDNA clone MtBC43E07 T3, mRNA
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Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Glaninazzi-Pearson
Medicago truncatula ESTs from endomycorrhizal roots
Unpublished (2000)
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BP 191 91006 EVRY cedex - France
Emall: seqreféqenoscope.cns.fr, Web: www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3']. CDNA was cloned into the XhoI and BamHI sites.
Vector: a modified pBluescript KS(+) after bulk excision
from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              888 AGGAAAATTCATCGCGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGATT 947 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 11
visit our web site (http://genome.rtc.riken.go.jp) for details.
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                                                                                                                                                                                                                                                                                                                                            /tissue_type="thymus"
/dev_stage="adult"
/lab_host="DH108"
                                                                          Location/Qualifiers
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Matches 51;
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Intraractices:

Anote="Vector: pBluescript pSK: Site_1: ECORI; Site_2:

XhOI; M. truncatula sterilised seeds were germinated for
72h at 25 C, before transplanting into a 1/3 Epoisses soil:
2/3 calcined Terragreen mix in the presence of onion
root fragments colonized by the arbuscular mycorrhizal
fungus Glomus intraradices (Schenck & Smith, isolate LPAB). The plants were watered every day and twice a week with
a modified nutrient Long Ashton solution without phosphate
but with a high level of nitrate. After 3 weeks RNA was
extracted from whole root systems. CDNA was prepared from
polyA+ enriched RNA. The colon Stratagene and packaged using
Gigapack Gold packaging extractes. Plasmids containing CDNA
inserts were mass-excised from phage stocks using ExAssit
helper phage and propagated in Solk cells. Clone ordering
and sequencing was performed by the Centre National de
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Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.

1 (bases 1 to 634)
McCarter,J., Clifton,S., Marra,M., Hillier,L., Kucaba,T., Martin,J., Mocarter,J., Clifton,S., Marra,M., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCant,R., Materston,R. and Wilson,R.
The Washington Univ. Nematode EST Project, 1999
Contact: McCarter JP
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                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="harvested 3 weeks post inoculation with Glomus intraradices"
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CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email : Mt-est@tolbouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html).
Location/Quallfiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     623 TCTTGTTTCGGCGTTTTATCGCGAACGGTGGCGAATTTGTATCTGCGCGTGTCATCGGCT 682
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                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="arbuscular mycorrhiza"
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                                                                                                                                                                                      /organism="Medicago truncatula"
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743 ATGCAG 748
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/clone_llb="Sommer Pristionchus"
/sex="predominantly hermaphroditic"
/dev_stage="mixed stages (embryo to adult)"
/dev_stage="mixed stages (embryo to adult)"
/deb_host="not applicable (host cell line)"
/note="vector: Uni-ZAP XR Vector (Stratagene); Site_l: 5'
/note-"vector: Uni-ZAP XR Vector (Stratagene); Site_l: Site_l
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 1800
Fax: 314 286 n800
Fax: 314 286 n800
Fax: 314 286 n800
Fax: 314 286 primer Constructed by Dr. Ralf Sommer DNA Sequencing by:
Washington University Genome Sequencing Center
Contact Dr. Ralf Sommer (Talf.sommer@tuebingen.mpg.de) for
information about this clone.
Seq primer: -40RP from Gibco
High quality sequence stop: 384.
Location/Qualifiers
1.634
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Medicago.
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Torter Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Imman, J.T., Weller, J. W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula drought library
Conpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE248875 676 bp mRNA EST 13-JUL-2000 NF023D11DT1F1091 Drought Medicago truncatula cDNA clone NF023D11DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1003 GCTCGAAAACTTCTTCCAGCCCTCGCGCCTGCGAGTTCTGAAGAACGATATTCCAAATGG 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     943 GAGTICGCIGGCICACAGCCGCICCIAACIGGAAACGIGCGCAIGTGCTCIAIACGCAC 1002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            295 GTGATGNCTCNNATCAACGCGGCCCGGACCTGGGATCNCGTCTCTTCGCTTTCTACCCGC 354
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Lotus japonicus
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fabales; Fabaceae; Papilionoideae; Lotus.

1 (bases 1 to 205)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a
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Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/dev_stage="young plants (two-week old)"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Plantlets"
/dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire plantlets harvested in a series of days post watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               683 TTGAGACTGAAGGTAGGCCCCTTAAAGGCATTACAACCACGACGGCGTTCTGGCCGTTC 742
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japonicus cDNA clone MWM232a12_r 5', mRNA sequence.
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                         The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Teal: 580 221 7391
Fex: 580 221 7391
Email: gdmay@noble.org
Medicago Genome Initiative accession: MGI:S:25465
Plate: 023 row: D column: 11
Seq primer: TCACACAGGAACAGCTATGAC.
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/db_xref="taxon:3880"
/clone="NF023D11DT"
/clone_lib="Drought"
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/db_xref="taxon:34305"
/clone="MWM232a12_r"
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DNA Res. 7 (2), 127-130 (2000)
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Plant Biology Division
The Samuel Roberts Nob.
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/note-"Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI; isolate-Miyakojima MG-20" 49 a 67 c 33 g 56 t
                                         BASE COUNT
ORIGIN
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ö 0; Gaps Query Match
2.7%; Score 34.6; DB 18; Length 205;
Best Local Similarity 59.8%; Pred. No. 15;
Matches 58; Conservative 0; Mismatches 39; Indels 0; ολ Q ò

QQ

Search completed: January 1, 2001, 01:12:46 Job time: 25785 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 ATGGCTGAGAACCACAAAAA......AAACGGGTCCGGCAAGTTAA 1296
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Database

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AR016594 115327 115326 115326 AR016591 115324 AR016595 115324 AR016595 115328 AR016595

Description

DB

SUMMARIES

121 GAAGGTGCATCGTTTGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 180 181 ATGCCGGAAACTTGACGAGGTGCCGAAGTGGCTCCTTGACCCGATGGGGCCGTTGTCA 240	241 ATCCGGTTCAGCTATTTCCAACCATCATGCCCTGGTTGATTCGCTTTTGTTGCCGGA 300 301 AGACCAACAACAAGAGGAGGAAAGCACTCGGAATCTCTATCATGCCGGGTG 360 111111111111111111111111111111111111	361 CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCATCCGCCATGAAGGT 420 	421 CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGGGAGGTTGGGAACTG 480 	481 CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCTGCGTGATGCTTTGCGTGATTTCGAT 540	541 CCTAACTIGICGCAIGCITTTACCAAGGGCATICITATAGAAGAGAACGGICACACGGIT 600 	601 AATCCGCAAGGGTCGTGACCCTCTTGTTTCGGCGTTTTTATCGCGAACGGTGGCGAATTT 660	661 GTATCTGCGCGTGTCATCGGTTTTGAGACTGAGGTCGTGCTCTCAAAGGCATTACAACC 720 	721 ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCTAAATCA 780 	781 CTTGCTAATTGGTAGGCGATGACATCCCGCTGGATACCGAACGTGGATATCATATCGTC 840 	841 ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACGATGCGTCAGGAAATTCATC 900	901 GCGACACCTATGCAAATGGGTCTTCGTGTTGCTGGTGTTGAGTTTGCTGGTCTCACA 960 	961 GCTGCTCCTAACTGGAAAGGTGGGCATGTGCTCTATACGCACGC	1021 GCCCTGGGGCTGGGAGTTCTGAAGAACGATATTCCAAATGGATGG	1081 ATTCCTGATTCTCTACAGTGATTGGTCGTGCAACTCGTACACCCGACGTAATCTATGCT 1140	1141 TITGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG 1200	1201 CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGT 1260 1201 CTCCTCGCAGGCGAAAAGACCTCAATCGACTTTTGCCCCTTCGCACCAACCGCTTTGGT 1260
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13 926.8 71.5 1631 5 A59869 A59869 14 87.4 6.7 3430 2 PSEKSDA M69158 Pseudomonas 15 69.2 5.3 2289 2 PSEKSDA M69159 Pseudomonas 16 69 5.3 69 5 AR016616 AR016616 Sequence 17 69 5.3 69 5 AR016619 Sequence 18 69 5.3 69 5 115349 I15349 19 69 5.3 69 5 115342 Sequence 20 68 5.2 68 5 AR016618 Sequence	68 5.2 68 5 115351 63.4 4.9 65 5 AR016614 63.4 4.9 65 5 115347 62 4.8 62 5 AR016613 62 4.8 62 5 AR016613 61 4.8 62 5 AR016613	61 4.7 61 5 115350 42.8 3.3 196999 57 AC073346 42.6 3.3 1586 98 MNUTO653 42.6 3.3 1598 88 MNUTO654	31 42 3.2 31202 37 AC013022 32 42 3.2 302357 29 AE003443 33 41 3.2 41 5 AR016615 34 41 3.2 41 5 T15746	40.4 3.1 186935 48 AC022322 40.2 3.1 840 89 CNSOLEDB 40.2 3.1 38914 2 MSCB937CS 40.2 3.1 179553 40 ACO320553	39.8 3.1 223469 56 AC069019 39.4 3.0 2767 54 EIMMAX 39.4 3.0 1612 88 MMU70652 30.3 0 47358 40 AC050141	45 39.8 3.0 34.20 38 ACO14160 44 39 3.0 235414 29 AE003708 45 38.8 3.0 1558 88 MMU70646	ALIGNMENTS	ARO16594 ARO16594 ARO16594 ARO16594 ARO16594 ARO16594 ARO16599 ARO16598	AR016594 GI:3972871	ORGANISM EFERENCE AITHORS	TITLE Glyphosate tolerant plants JOURNAL Patent: US 5776760-A 7 07-JUL-1998; FEATURES Location/Qualifiers	OUNT 287 a	Query Match Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1296; Conservative 0; Mismatches 0; Indels 0; Gans 0.	ATGCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60	61 GCTTTGATGCTTCAACGCGGGGATCACTTGATGCTTGATGCTTGATTGA	121 GAAGGTCCATCGTTGGGAATGCCGATCGTTCAACGGGTCATCCGTCGTCGTTGTGTTCTCGTCGTTCTTGTCTTCACGGGTCATCGTCGTCGTTGTTGTTCTTCTTGTTGTTCTTCTTGTTGT

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                              ATCGCGAATCCGGAAGCCGCTCCACCATTCCGACGACGCATCAGGAAAATTCATC
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                    GTATCTGCGCGTGTCATCGGTTTTTGACACTGAAGGTCGTGCTCTCAAAGGCATTACAACC
                                                             ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCTAAATCA
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Barry, G. Francis and Kishore, G. Murthy.
Glyphosate tolerant plants
Patent: US 5776760-A 6 07-JUL-1998;
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95.48;
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Best Local Similarity 95.4
Matches 1237; Conservative
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1 (bases 1 to 1296)
Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 7 31-OCT-1995;
Location/Qualifiers
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Sequence 7 from patent US 5463175.
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	CCTCCTGGC 120 	CCTATGTCC 180 	CCGTTGTCA 240 CCGTTGTCA 240	TTAGCCGGA 300 TTAGCCGGA 300	TCCACGGTG 360 TCCACGGTG 360	CATGAAGGT 420 	TGGGAACTG 480 TGGGAACTG 480	GATTTCGAT 540 GATTTCGAT 540	CACACGATT 600 CACACGATT 600	3GCGAATTT 660 3GCGAATTT 660	ATTACAACC 720 ATTACAACC 720	ICTAAATCA 780 CGAAATCA 780	CATATCGTC 840 	AAATTCATC 900 	3GTCTCACA 960 	CTTCTTCCA 1020	GTCCTAGC 1080 	r 114
	CTTGATTGACCCGAACC 	CGGCTCATCCGTCGTCC 	CCTTGACCCGATGGGGC 	STTGATTCGCTTTCTGT 	CCGCAATCTCATCAAGI 	SAGCCATCTGATCCGCC 	CAAGGACCGCGGAGGTT 	rgctgatgctttgcgtg 	IATAGAAGAGAACGGTC 	TTTTATCGCGAACGGTG 	rcgtgctctcaaaggca 	FGCAGCTGGTGCACACT 	raccgaacgtggatatc 	SACCGATGCGTCAGGAA 	ractgttgagtttgctg 	racgcacgctcgaaaac 	2AAATGGATGGGTTTTC 	rcgtacacccgacgtaa
	CGTGGATTCAAAGTCAC 	AATGCCGGATGCTTCAA(AGCGTGCCGAAGTGGCT 	CCAACCATCATGCCCTG(BAGCAGGCGAAAGCACT(GCGAGGAGGCTGATGCC 	3GAGAAGCAGACTTCGCC 	GGCAGGCAGATCCTCTCT 	TTTACCAAGGGCATTCT! 	ACCCTCTTGTTTCGGCG'	GGTTTTGAGACTGAAGG7 	STTGATGCAGCTGTTGT 	GATGACATCCCGCTCGA1 	SCTCCACGCATTCCGACC 	GGTTTCGTGTTGCTGG1 	CGTGCGCATGTGCTCTAI	rctgaagaacgatattcc 	STGATTGGTCGTGCAACT
	GCTTTGATGCTTCAACGTCGATGGATTCAAAGTCACCTTGATTGA	GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCGTCTTATGTCC 	atgccgggaaacttgacgagcgtgccgaagtggctccttgacccgatggggcgftgtca 	ATCCGGTTCAGCTATTTCCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGA 	AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGG' 	CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCGCCATGAAGGT 	CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTG 	CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCTGCTGGTGATGCTTTGCGTGATTTCGAT 	CCTAACTIGICGCAIGCITITACCAAGGGCATICITATAGAAGAGAACGGICACACGAT 	AATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCGTTTTTATCGCGAACGGTGGCGAATT 	GTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACC 	ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACTCTAAAT 	CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGT 	ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACGATGCGTCAGGAAAATTCAT 	GCGACACCTATGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACA 	GCTGCTCCTAACTGGAAACGTGCGCATGTGCTCTATACGCACGC	GCCCTCGCGCCTGCGAGTTCTGAAGAACGATATTCCAAATGGATGG	ATTCCTGATTCTCTTCCAGTGATTGGTCGTGCAACTCGTACACCCGACGTAATCTATGCT
-	61	121	181	241	301	361	421	481	541 (601	661 (721	781 (841 /	901 (961 (1021 0	1081
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M Unknown.

E 1 (bases 1 to 1296)

S Barry.G.F. and Kishore,G.M.

Glyphosate tolerant plants

AL Patent: US 5463175-A 6 31-OCT-1995;

Location/Qualifiers

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"unknown" 281
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Pred. No. 0;
0; Mismatches
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6 from patent US 5463175
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Local Similarity 95.4%;
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BASE COUNT 381 a 480 c 469 g 361 t 1 others ORIGIN	ery Match 92.3%; Score 1196.8; DB 5; Length 1692; st Local Similarity 95.2%; Pred. No. 0;	Marches 1234; Conservative U; Mismarches 52; Indels U; Gaps 1 ATGGCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60	12	121 GAAGGTGCATCCTTTGGAATGCCGGAATTCAAAGTCACCTTGATTGA	240 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCC 29 181 ATGCCGGGAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCGGATGGGGCCGTTGTGT 24	Db 300 ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGGGCCCGTTGTCA 359 Oy 241 ATCCGGTTCAGCTATTTTCCAACCATCATGCCTGGTTGATTCGCTTTGTTAGCCGGA 300 Db 360 ATCCGGTTGAGCTATTTTCCAACCATCATGATTGATTCGTTTGTTT	301 AGACCAAACAAGGTAAGGAGGAGGCAAAAGCACCCCCAATCTCATCAAGTCCACGGTG 36 111111111111111111111111111111111111	361 CCTCTGATCAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCGCCATCAAGGT 42 [421 CATCTGACGTATATCGTGGAGAGAGACTTCGCCAAGGACCGGGGGGTTGGGAACTG 48 [1] IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	940 CATCIONCOGININCINGAGANACIACATICOCCANGGACCIGGGGAACTG 59 481 CGGCGTCTCAACGGTGTTCGCACGCAGATCCTCTGCTGCTGATGATGGTGATTCGAT 54 111111111111111111111111111111111111	541 CCTAACTTGTCGCATGCTTTTACCAAGGCATTCTTATAGAAGAGAACGGTCACGCGATT 60 560 CCGAACTTGTCGCATGCTTTTACCAAGGCATTCTTATAGAAGAGAACGGTCACACGATT 60 660 CCGAACTTGTCGCAACGCATTCAACAAGAAAAAGATAAAAAAATAAAAAAAA	601 AATCGCAAGGCTCGTGACCTTTTTCGCCGTTTTTATCGCGAACGGTGGCGAATTT 66 111111111111111111111111111111111	GTATCTGCGCGTGTCATCGGTTTTGAGACTGGAGGTCGTCTCTGAAAGGCATTACAACC 72	Qy 721 ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCTAAATCA 780	Oy 781 CTTGCTAATTCGCTAGGGGATGACATCCGGATACCGAAGGTGGATATCATATCGTC 840	QY 841 ATCGCGAAACCGGAGCGCTCCACGCATTCCGACGACGATGCGTCAGGAAAATTCATC 900 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 901 GGGACACCTATGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACA 960	Qy 96.1 GCTGCTCCTAACTGGAAACGTGCGCATGTGCTCTATACGCACGC
	Qy 541 CCTAACTTGFCGCATGCTTTTACCAAGGCATTCTTATAGAAGAGAACGGTCACACGATT 600 	Oy 601 AATCCGCAAGGCTCGTGACCCTCTTGTTTCGGCGTTTTTATCGCGAACGGTGGCGAATTT 660 11111111111111111111111111111111111	OY 661 GTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACC 720 	Oy 721 ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGCAGCTGGTGCACACTCTAAATCA 780 	OY 781 CTTGCTAATTCGCTAGGGGATGACATCCCGCTCGAACGTGGATATCATATCGTC 840 	OY 841 ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACCGATCGTCAGGAAAATTCATC 900 11111111111111111111111111111111111	901 GGGACACCTATGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACA	Oy 961 GCTGCTCCTAACTGGAAACGTGCGCATGTGCTCTATACGCACGC	<pre>QY 1021 GCCCTCGCGCCTGCGGGTTCTGAAGAACGATATTCCAAATGGATGG</pre>	Qy 1081 ATTCTGATTCTTCCAGTGATTGGTCGTGCAACTCGTACACGCGACGTAATCTATGCT 1140	Oy 1141 TTTGGTCACGGTATGGCAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG 1200 1141	OY 1201 CTCCTCGCAGGCGAAAAGACCTCAATCGACATTCGCCCTTCGCACCAAACCGCTTTGGT 1260	Oy 1261 ATTGGCAAATCCAAGGGTCGGCAATTAA 1296 	RESULT 5 AR016591 AR0	AR016591 AR016591.1	NISM	TITE Glyphosate tolerant plants JOURNAL Patent: US 5776760-A 3 07-JUL-1998; FEATURES Location/Qualifiers	source 11092 /organism="unknown"

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1 (bases 1 to 1293)

Barry, G.Francis and Kishore, G.Murthy.

Glyphosate tolerant plants

Patent: US 5776760-A 4 07-JUL-1998;

Locallon/Qualifiers
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Pred. No. 0;
0; Mismatches
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95.0%;
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Best Local Similarity 95.0
Matches 1231; Conservative
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1138 TTCGGCCATGGTCATCTCGGCATGACAGGGCGCCGATGACCGCTAACGCTCAGAG
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ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACGATGCGTCAGGAAATTCATC
                                    GCGACACCTATGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACA
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Pred. No. 0;
0; Mismatches
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 3 31-OCT-1995;
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Matches 1231; Conservative
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Pred. No. 0;
0; Mismatches
                1 (bases 1 to 1293)
Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 4 31-OCT-1995;
Location/Qualifiers
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                                                                    /organism="unknown"
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Best Local Similarity 95.0
Matches 1231; Conservative
        Unclassified.
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Pred. No. 2.8e-277;
0; Mismatches 178;
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rry,G.Francis and Kishore,G.Murthy
rphosate tolerant plants
tent: US 5776760-A 8 07-JUL-1998;
Location/Qualifiers
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quence 8 from patent US 5776760.
316595 GI:3972872
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Db 61 GCTTTGATGCTTCAAGGTGTGATCTTGATTGATTGATCCAAACCCACGGT 120 Qy 121 GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAAGGCTCATCCGTCGTCCTCTTTCC 180		Qy 541 CCTAACTTGTCGCATGCTTTACCAAGGCATTCTTATAGAAGAACGTCACACGATT 600 Db 111111111111111111111111111111111111	QY 781 CTTGCTAATTCGCTAGGCGATGACCGCTCGATACCGAACGTGGATATCATATCGTC 840 DD 111111111111111111111111111111111111	OY 1021 GCCCTGGGGCTGCGAGTTCTGAAGAACGATATTCCAAATGGATGG
			115328.1 GI:1250236 115328.1 GI:1250236 Unknown. Unclassified. 1 (bases 1 to 1296) Barry, G.F. and Kishore, G.M. Glyphosate tolerant plants Patent: US 5463175-A B 31-OCT-19 Location/Qualifiers 1. 1296 / organism="unknown" 271 a 359 c 305 g 3	Query Match 78.0%; Score 1011.2; DB 5; Length 1296; Best Local Similarity 86.3%; Pred. No. 2.8e-277; Age-277; Matches 1118; Conservative 0; Mismatches 178; Indels 0; Gaps 0; Qy 1 ATGGCTGAGAACCACAAAAAGTAGGCATGGCTGGAGCTGGAGTGGTGGTGTTGGTGTTGGCT 60 Intellitititititititititititititititititit

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                     541 CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAACGGTCACACCATC
                                                                                                                       ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCTAAATCA
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                                                                     GTATCTGCGCGTGTCATCGGTTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACC
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 17 31-0
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Pred. No. 6.6e-276;
0; Mismatches 181; I
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Barry,G.Francis and Kishore,G.Murthy.
Glyphosate tolerant plants
Patent: US 5776760-A 17 07-JUL-1998;
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Best Local Similarity 86.0%; Pred. No. 6.6e-276; Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0; Matches 1115; Conservative 0; Mismatches 181; Indels 0; Gaps 0; Or 1	0y 241 ATCCGGTTCAGCTATTTCCAACCATCATGCCTGGTTGATTCGCTTTTTTTT	0 AATCCGCAAGGGCTCGTGACCTCTTGTTTCGGGATTTTATCGCGAACGGTGGCGAATTT 660

ketoglutarate semialdehyde dehydrogenase. Pseudomonas putida DNA.

GI:150981

M69158.1

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PSEAKSD 3430 bp DNA BCT 26-APR-1993 Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase gene, complete cds.

LOCUS

RESULT 14

PSEAKSD

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MLTPGIFSAYOGSVGGLAGNANAQAAASGQAGGPROQRDIDBARALLPFLERRAGRIL
WNGRTGGENGVACASDEQVHUNAEHLEGQLTATLQCDDADIDBARALLPFLERRAGRIL
WNGRTGGEVCDANNIGGFPFATSDARTTSVGTAAILRFLRPVCYQDFPNALLPQALQ l (bases 1 to 3430) Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C. Nucleotide sequences of hydroxyproline-specific alpha ketoglutarate semialdehyde dehydrogenase genes from two strains of pseudomonas ŝ 2327 2447 2567 2626 gamma subdivision; Pseudomonas group; 142 202 262 322 382 442 501 Gaps 2208 TCGCCGTGGTGGGCGCCGGGATTGTCGGCGTTGCCTGTGCCCTGCAACTGGCCCGCCAGG GATTCAAAGTCACCTTGATTGACCCGAACCCTCGTGGCGAAGGTGCATCGTTTGGGAATG 23 TAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACTGCTTTGATGCTTCAACGTCGTG GCTCGATCGGCGCGCAGCACTGTTCCAGGAGGATGGTTCGTTGCTGTGTTCTTCTTCAGAGAAG CCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGAAGACCAAACAAGGTGAAGGAGC 323 AGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGCGG GTGTGGCCGGCATCCGCACGCTGAACGAAGCAGCCTGGGTGCATGGCAGCGCCTGGTGG CCGGATGCTTCAACGGCTCATCCGTCGTCCTATGTCCATGCCGGGAAACTTGACGAGCG 203 TGCCGAAGTGGCTCCTTGACCCGATGGGGGCCGTTGTCAATCCGGTTCAGCTATTTTCCAA AGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCGTGGAG 443 AAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTGC-GGCGTCTCAACGGTGTTCGC 603. .2180 /gene="ketoglutarate semialdehyde dehydrogenase" 603. .2180 603. .2180 /gene="ketoglutarate semialdehyde dehydrogenase" /codon_start=1 6 Length 3430; 506; Indels Score 87.4; DB 2; Pred. No. 8.6e-14; 0; Mismatches 506; /organism="Pseudomonas putida' /db_xref="taxon:303" 571 t ed (1991) Location/Qualifiers 1. .3430 1157 g HGNPLOLRRLLDGKREG /transl_table=11 Bacteria; Proteobacteria; Query Match 6.7%; Best Local Similarity 46.6%; Matches 450; Conservative 1140 c Pseudomonas putida Pseudomonas. Unpublished ø 562 putida VERSION KEYWORDS SOURCE ORGANISM source BASE COUNT ORIGIN AUTHORS TITLE JOURNAL FEATURES 143 263 2448 2508 383 gene 83 REFERENCE CDS g g 9 Dp g g qq à à ò ó õ ò ò ð

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Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
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Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase
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/protein_id="AAA25870.1"
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PLAFSYVAGODTASALAAGCPVAVKAAISAHPOTSELJVGRAVARAVORSALPEGVESLLF
GSGREVGIALVSDPRIKAVGFTGSRSGGMALINAAQARLEPIPVYAEMSSINPVLLIP
AALEARGEAALAGGFVASLTYGAGAGGFTONFGLVAMRAGGPALDAFIKAAANLVORSPAOT
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MFGAASLIVOCASDDEIRQVTEHLEGGLTATLHLDDADLESARALLPVLERKAGRLLV
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                                                                                    The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme which has been modified using mutagenic primers. The gene sequence was redesigned to eliminate as much as possible the following sequences or sequence features (while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more; A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + C% of the GOR gene was reduced from 56% in the manipulated version (Q20833) to 52% in the manipulated version that wild type GOR enzyme. It was obtd. From bacterial isolate LBAA.

It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant.

Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively. controlled in fields contg. crops.
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 Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate
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0; Mismatches
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/note= "encodes wild type glyphosate oxidoreductase"
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GTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACC
                   gtatctgcgcgtgtcatcggttttgagactgaaggtcgtgctctcaaaggcattacaacc
                                      ACTAACGGTGTTCTGCCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACCTCTAAATCA
                                               CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC
                                                                                                                                                       GCGACACCTATGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACA
                                                                                                                                                                           gogacacctatggaaatgggtcttcgtgttgctggtactgttgagtttgctggtctcaca
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                                                                                                                                                                                                                                                                                                              TTTGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG
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                                                              ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCTAAATCA
                                                                        ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACGGATGCGTCAGGAAAATTCATC
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                     GTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACC
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/note= "glyphosate oxidoreductase coding reglon"
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                                                                                                                                         The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme which has been manipulated such that it is suitable for introduction into and expression in plant transformation vectors, but it still encodes the wild type GOR enzyme. It was obtd. from bacterial isolate LBAA. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant. Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops. See also Q20832-Q20841 and Q22705.
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                                                                                                                                                                                                                                                                                 Length 1321;
                                                                               Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                   Sequence 1321 BP; 292 A; 373 C; 369 G; 287 T; 0 other;
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Pred. No. 0;
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95.48;
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                              Barry GF;
                                                WPI; 1992-041559/05.
P-PSDB; R20642.
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24-JUN-1991; 25-JUN-1990;

Kishore GM,

WO9200377-A

09-JAN-1992

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                                                                                                    CCTAACTTGTCGCATGCTTTTACCAAGGGCATTCTTATAGAAGAGAACGGTCACACGATT
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/note= "not present in alternative sequence"
                                                                                                                                                                                                                                                                                                     Gene encoding glyphosate oxido-reductase enzyme - used to transform plants to produce plants tolerant to glyphosate herbicide
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92.1%; Score 1193.6;
Best Local Similarity 95.1%; Pred. No.0;
Matches 1232; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 2; 142pp; English
                                                                                                                                  91US-0717370
90US-0543236
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                                                                                                                                                                                                                    Barry GF;
                                                                                                                                                                                   (MONS ) MONSANTO CO.
                                                                                                                                                                                                                                                    WPI; 1992-041559/05.
P-PSDB; R22262.
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                                                                                                     CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCCCTATGTCC 180
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/note= "glyphosate oxidoreductase coding region"
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/note= "in the alternative sequence C is
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Pred. No. 0;
0; Mismatches
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/note= "in the alternative
ocation/Qualifiers
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94.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1992-041559/05.
P-PSDB; R20642.
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Transformed plants resistant to glyphosate can be obtd. so that they express the controlled in fields contg. crops.
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86.3%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel sugar beet plant, including its descendants expressing 5-enoloyruvylshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capa of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
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                                                                                                                                                                                Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;
5-enolpyruvylshlkimate-3-phosphate synthase; transgenic; herbicide;
tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glyphosate resistant transgenic sugar beet plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1011.2;
Pred. No. 0;
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Sugar beet T-DNA containing cp4/epsps #2
                                                                                                                                                                                                                                                                                                                                                                       (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES
                                                                                                                                                                                                                                                                                                                                                                                                                 pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 15; Page 36-41; 55pp; English.
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                                                                              BP
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86.3%;
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                                                                              8418
                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                               Steen P,
                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-313347/26
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                                                                             X57309 standard;
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                                                                                                                                                                                                                                        Beta vulgaris
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                                                    RESULT
X57309
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A chemically inducible plant gene expression cassette which comprises an inducible promoter linked to a gene (I) that confers resistance to a herbicide, is calaimed. (I) imparts resistance to N-phosphonomethyl.

Glycine (glyphosate) or its salts, but may also be a gene for resistance to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolones, cet. The inducible promoter (e.g. alch, alck, alch or other alck-induced gene promoter) is operatively linked to an alck regulator sequence.

Induced expression of (I) avoids the risk that constitutive expression of (I) avoids the risk that constitutive expression of controlled by herbicide applied without inducer and minimises the chance that herbicide-resistant strains of weeds will arise. The expression cassette is strictly controlled and suitable for general use in plants (both mono- and dicotyledons). The alchAalck gene switch was exemplified with genes conferring resistance to glyphosate. The switch was used to sylthogen inducible expression of glyphosate oxidase (GOX) in plants.

Switchable GOX was expressed alone or in conjunction with constitutive expression of 5-enol-pyruvylshikimate 3-phosphate (BPSPS) CP4. Constructs were optimised for expression in mono- and dicotyledonous crop species. The present sequence comprises a fusion of the COX gene fused to the chloroplast transit sequence a from Arabidopsis RUBISCO (CPT1). This sequence was ligated into pwJB1 (see T8566) and used in construction of
                                                                                                                                                                  expression cassette; inducible promoter; alcA; alcA; regulator; alcAol dehydrogenase; herbicide resistance gene; glyphosate; n-phosphonomethyl-glycine; glyphosate, GOX; EPSPS; 5-enol-pyruvylshikimäte 3-phosphate CP4; chloroplast transit sequence 1; Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemically inducible cassette for expressing herbicide resistance gene in plants - and derived plants, partic. for resistance to glyphosate, avoids constitutive expression and minimises development
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BP
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  1631
                                                                                   (first entry)
DNA;
                                                                                                                                                                                                                                                                                               Chimeric Arabidopsis
                                                                                                                             CPT1-GOX gene fusion
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T85664 standard;
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1 ATGGCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT

1053 1030 1413 1113 1173 1233 CTCTTCCAGTGATTGGTCGTGCAACTCGTACACCCGACGTAATCTATGCTTTTGGTCACG 1150 790 453 223 335 395 693 455 753 515 813 575 635 933 695 993 574 gttgattcgtttcttgcttgctggaagaccaaacaaggtgaaggagcaagctaaggcact GAGCCATCTGATCCGCCATGAAGGTCATCTGACCGTATATCGTGGAGAGAGCAGACTTCGC 1234 tggagatgggtcttcgtgttgctggaaccgttgagttcgctggtctcactgctgctcta 1294 actggaagcgtgctcacgttctctacactcgtgctcgtaagttgcttccagctctcgctc ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACC---------------CGATGGGGCCGTTGTCAATCCGGTTCAGCTATTTTCCAACCATCATGCCCTG GTTGATTCGCTTTCTGTTAGCCGGAAGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACT CCGCAATCTCATCAAGTCCACGGTGCCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGC 754 caaggaccgtggaggttgggaacttcgtcgtctcaacggtgttcgtactcaaatcctcag TGCTGATGCTTTGCGTGATTTCGATCCTAACTTGTCGCATGCTTTTACCAAGGGCATTCT 814 cgctgatgcattgcgtgatttcgatcctaacttgtctcacgcctttaccaagggaatcct 576 TATAGAAGAACGGTCACACGATTAATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCG 636 TTTTATCGCGAACGCTGCCGAATTTGTATCTGCGCGTGTCATCGGTTTTTGAGACTGAAGG TCGTGCTCTCAAAGGCATTACAACCACTAACGGTGTTCTGGCTGTTGATG-----CGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTCGTCATCGCGAATC 1114 ccettggtgatgacatcccattggataccgaacgtggataccacatcgtgatcgccaacc CGGAAGCCGCTCCACGCATTCCGACGACGATGCGTCAGGAAAATTCATCGCGACACCTA ACTGGAAACGTGCGCATGTGCTCTATACGCACGCTCGAAAACTTCTTCCAGCCCTCGCGC CTGCGAGTTCTGAAGAACGATATTCCAAATGGATGGGTTTTCGTCCTAGCATTCCTGATT TGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACAGCTGCTCCTA 216 334 394 181 454 514 276 396 969 791 971 121 224 336 1031 1354 1091 746 851 911 ò a ò q g ò q Ob g g g qq ò ò ò ò ò q δ ò q ò ò P ö pp g g δ ò ò ð ò

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            ATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGGGCCGTTGTCA
                                                                                                                                                   AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
                                                                                                       ATCCGGTTCAGCTATTTTCCAACCATCATGCCCTGGTTGATTCGCTTTCTGTTAGCCGGA
                                                                                                                                                                                                CCTCTGATCAAGTCATTGGCGGAGGAGGCTGATGCGAGCCATCTGATCCGCCATGAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel sugar beet plant, including its descendants expressing 5-anolpyruvjehikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
                                                                    GCGAAAAGACCTCAATCGACATTTCGCCCTTCGCACCAAACCGCTTTGGTATTGGCAAAT 1270
                                                                                1414 cccttccagtgattggtcgtgctacccgtactccagacgttatctacgctttcggtcacg 1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7205 atggctgagaaccacaagaaggttggtatcgctggagctggaatcgttggtgtttgcact 7264
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                                                                                                                                                                                                                                                                                      Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; 9lyphosate; Roundup; N-phosphonomethyl-glycine; ss.
                                  GTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAGCTCCTCGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 8798;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54.2%; Score 703; DB 20; Length 86.3%; Pred. No. 6.9e-213;
1ve 0; Mismatches 135; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glyphosate resistant transgenic sugar beet plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                                                                                                                                Sugar beet T-DNA containing cp4/epsps.
                                                                                                                            1271 CCAAGCAAACGGGTCCGGCAAGTTAA 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pp;
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Matches 784; Conservative
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                       CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGAACTG
                                                                                                                                     caccttaccgtgtaccgtggagaagcagacttcgccaaggaccgtggaggttgggaactt
                                                                                                                                                                                                          gtgtctgctcgtgttatcggattcgagactgaaggtcgtgctctcaagggtatcaccacc
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                                                                                                                                                                                  CGGCGTCTCAACGGTGTTCGCACGCACATCCTCTCTGCTGATGCTTTGCGTGATTTCGAT
                                                                                                                                                                                                                                                                          CCTAACTTGTCGCATGCTTTTACCAAGGGCATTCTTATAGAAGAGAACGGTCACACGATT
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7716 aacccacaaggictogigactcitigiticgicgiticatogiaacggiggagagic 7775
                                                                                                          661 GTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACC
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1632..1637
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cerevisiae.
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Lippard SJ,
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                                                                                                                                                                                                                                                                              descendants expressing 5-enolpyruvyjshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7415
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                                                                                                                                                                                                                                                                  This invention describes a novel sugar beet plant, including its
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 20; Length 8012;
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8012 BP; 2096 A; 1855 C; 1879 G; 2182 T; 0 other;
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                                                                                                                                                                                                              Glyphosate resistant transgenic sugar beet plants
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 54.2%; Score 701.8; DB 20; Best Local Similarity 86.4%; Pred. No. 1.6e-212; Matches 775; Conservative 0; Mismatches 122;
                                                                                                                 (NOVS ) NOVARTIS AG. (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH
                                                                                                                                                            PP;
                                                                                                                                                                                                                                       Claim 8; Page 24-29; 55pp; English.
                                                                                                                                                           Tenning
                                                                 98WO-EP06859
                                                                                        97US-0112003
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                                                                                                                                                           Steen
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                                                                                                                                                           Mannerloef M,
                                                               29-OCT-1998;
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                                      14-MAY-1999
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                                                                                                                                                                                                                                                                                                    Structure-specific recognition protein; SSRP; yeast; DM 3002; library; open reading frame; highly charged domain; DM 1001; human; high mobility group protein; polyadenylation signal; ss.
                                                                                                       897
                                                                 721 ACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCTAAATCA
                                                  781 CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying c-DNA encoding eukaryotic DNA structure-specific recognition protein - by screening expression prods. of library using labelled oligo-nucleotide probe then detecting prod.
                                                                                                                  7956 atcgccaacccagaagctgctccacgtattccaactaccgatgcttctggaaagttc
                                                                                                      841 ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACCGATGCGTCAGGAAAATTC
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Toney JH;

Pil PM,

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bp. An open reading frame contiguous with the reading frame for the beta-galactosidase gene of lambda phage was found in the lambda-yPt DNA sequence. The polyadenylation signal is the same as that found in 50% of S. cerevisiae genes. Translation of the open reading frame yields an amino acid sequence of 534 residues. This peptide sequence is known as fractional ySRP (fySSRP). fySSRP contains eight runs of five or more Glu residues, of which the longest contains fifteen residues. The sequence contains a total of 110 Glu residues which comprises one fifth of the total. Fifty Asn residues accounts for
                                                                                                                                                                                                                                                                                            CACTCTAAATCACTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGA 828
                                                                                                                                                                                                   649 GGTGGCGAATTTGTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAA 708
                                                                                                                                                                                                                        817 GATGATGATGTTGTTGAAGTTGTTGTTGTTGCAACTGGTGTTGCTGTTGTAGCT 758
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                                                                                                                                                                                 Gaps
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/product= SSRPl
/note= "DNA structure specific recognition protein"
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0
                                                                                                                                                          Score 37.4; DB 14; Length 3292; Pred. No. 0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      screening: anticancer drug; cytotoxic; genomic lesion; yeast;
chemotherapeutic agent; genotoxic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA structure specific recognition protein; SSRP1; cisplatin;
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                                                                                                                                                                                 Indels
                                                                                                                        Sequence 3292 BP; 1095 A; 768 C; 530 G; 899 T; 0 other;
                                                                                                                                                                              96;
                                                                                                                                                                              Mismatches
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                                                                                                    another 9.2% of the amino acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cerevisiae SSRP1 genomic DNA
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0
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88US-0247774.
89US-0410981.
90US-0539906.
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ID V09625 standard; DNA; 3292
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                                                                                                                                                                                Conservative
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                                                                                                                                                                Local Similarity
es 95; Conserv
                                                                                                                                                                                                                                                                                                                                                             TGGCATTTCCT
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22-SEP-1988;
22-SEP-1989;
18-JUN-1990;
26-DEC-1991;
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                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCATTACAACCACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCA 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  697 GGTGGTGAGTCAATTGAGGTTGCAGATTGGGTGGTAACAAACCAGGATGAGTAGCGGTGT 638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          817 GATGATGATGTTGTTGTTGAAGTTGTTGTTGTTGTTGCAACTGGTGTTGCTTGTTGTTAGCT 758

    using structure-specific

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           757 GCTGCTGTTGCTGCACTGCTGTTGTTGTAATTGCAGCTGTTGCATCTGCATCTGCTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3292 BP; 1095 A; 769 C; 530 G; 898 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37.4; DB 19;
Pred. No. 0.16;
0; Mismatches 96;
                                                                             DNA-binding agents
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                                                                                                                                                                   Disclosure; Column 47-54; 37pp; English
                                                                                                             recognition protein with HMG domain
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ID Z45602 standard; cDNA; 6558
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                                                                                   Cytotoxicity assay for
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95; Conserva
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WPI; 1998-086133/08
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Best Local S:
Matches 95;
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                                                                                 The present sequence represents the CDNA sequence of the murine OPA gene. The human OPA gene is derived from the PCTG4 region of chromosome X413. Polymorphism in this region are associated with mental retardation, autism, depression, bipolar affective disorder or hypothyroidism. One 12 bp insertion polymorphism occurs within the coding region of the human OPA gene, and introduces a 4 amino acid insertion in a putative OPA domain. This domain has been shown to be involved in tissue specific expression. Another Polymorphism consists of a pentanuclectide repeat approximately 7 kb upstream of the 12 bp polymorphism. Another polymorphisms consists of a pertanuclectide repeat approximately 7 kb upstream of the 12 bp polymorphism. The specification describes a method for screening for polymorphisms in a percification describes a method for screening for polymorphisms in a percification describes a method for screening for polymorphisms in a percification describes of the X chromosome have polymorphisms associated with neuropsychiatric disorders. The methods can be used to serve for the presence of a heritably linked form of methods can be used to a percification of the X chromosome have polymorphisms associated with neuropsychiatric disorders. The methods can be used to a peritably linked form of methods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polyhedrin promoter; expression vector; human; collagen; insect cell; Spodoptera frugiperda; Sf9; hydroxylate; proline; triple strand; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nan collagen expression vector for transfection of insect host ich is capable of hydroxylating collagen proline gps., resulting expression of stable triple stranded collagen molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    709 GGCATTACAACCACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGCAGCTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector pAC3A1 contg. human collagen type III alpha-1 chain gene.
              polymorphisms in the PCTG4 region of Xq13 for
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                                                                                                                                                                                                                                                                                                                                       retardation, autism, depression, bipolar affective disorder or
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 6558;
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6558 BP; 1637 A; 1801 C; 1644 G; 1475 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              2.8%; Score 35.8; DB 21;
1larity 56.3%; Pred. No. 0.75;
Conservative 0; Mismatches 52;
                              retardation or autism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example B3; Page 11-12; 16pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T16508 standard; cDNA to mRNA; 5460 BP
                                                           Example 7; Page 78-81; 100pp; English.
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Best Local Similarity
Matches 67; Conserv
              Identification of
                              diagnosing mental
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This is the nucleotide seqence of the expression vector pAC3A1 contg. the gene encoding the human collagen type III alpha-1 chain. The collagen gene is under control of a synthetic polyhedrin promoter (T16503-6) and is linked to the mellitin signal peptide sequence for ease of purification. The vector is used to express human collagen in insect cells, sep. Spodoptera frugiperda Sf9 cells. The cells have the ability to hydroxylate prolines in the collagen which is produced as a triple stranded molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       986 ATGTGCTCTATACGCACGCTCGAAAACTTCTTCCAGCCCTCGCGCCTGCGAGTTCTGAAG 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1154 gtgaagttggacctgcagggtctcctggttcaaatggtgcccctggacaaagaggagaac 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1106 GTCGTGCAACTCGTACACCCGACGTAATCTATGCTTTTGGTCACGGTCATCTCGGTATGA 1165
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                                                                                                                                                                                                                                                    Sequence 5460 BP; 1327 A; 1314 C; 1544 G; 1275 T; 0 other;
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                                                                                                                                                                                                                                                                                                                            Score 35.6; DB 17;
Pred. No. 0.79;
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N50025 standard; DNA; 501
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us-08-484-274-7.rng

transformed bacteria, with improved antiviral,

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plasmid transformed bacteria, with improved antivanti-proliferative and immune regulating actions
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                                                                                                                                 They are also easier to recover from incubation mixts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence encoding new modified human beta interferon polypeptides
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  βy
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   prepd.
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                                                                                                                                                                                                                  Indels
New modified human beta interferon polypeptide(s) · pr
plasmid transformed bacteria, with improved antiviral,
anti-proliferative and immune regulating actions
                                                                                                                                                        Sequence 501 BP; 112 A; 30 C; 69 G; 85 T; 205 other;
                                                                                                                                                                                         2.7%; Score 35.4; DB 6;
28.9%; Pred. No. 0.24;
ative 50; Mismatches 120;
                                                Claim 28; Chart 2c, page 34; 71pp; English
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1..501
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N50023 standard; DNA;
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                                                                                                                                 stability.
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                                                                                                                                                                                                                                                                                                                                     Gaps
                                            Compared with interferon beta prepd. by recombinant methods, the INFs of the invention are more active and have different affinities for cell surface receptors (allowing selective targetting); they have higher therapeutic index; improved stability against microbial breakdown during synthesis; and better in vivo solubility and stability. They are also easier to recover from incubation mixts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565 AAGGGCATTCTTATAGAAGAAGGGTCACACGATTAATCCGCAAGGGCTCGTGACCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       625 TTGTTTCGGCGTTTTATCGCGAACGGTGGCGAATTTGTATCTGCGCGTGTCATCGGTTTT
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                                                                                                                                                                                                                                                                                       Length 501;
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                                                                                                                                                                                                                Sequence 501 BP; 107 A; 31 C; 69 G; 80 T; 214 other;
                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                    Score 35.2; DB Pred. No. 0.28;
Claim 28; Chart 2a, page 32; 71pp; English
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                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
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Sequence 7, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 20, Appl
Sequence 9, Appl
Sequence 144, Appl
Sequence 144, Appl
Sequence 144, Appl
Sequence 144, Appl
Sequence 5, Appll
Sequence 5, Appll
Sequence 15, Appll
Sequence 5, Appll
Sequence 5, Appll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
US-07-814-964-12
US-08-228-442-12
US-08-328-442-12
US-08-328-463-14
US-08-232-463-14
US-08-728-463-14
US-08-728-51-9
US-08-698-551-9
US-08-698-551-9
US-08-698-551-9
US-08-698-551-9
US-08-533-901B-9
US-08-533-901B-9
US-08-873-9718-9
US-08-873-179-144
US-08-874-138-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-655-086-1
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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: HOETNET, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                     5273901-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5463175
GENERAL INFORMATION:
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Best Local Similarity
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5D_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
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Sequence 7, Application US/08484274A Patent No. 5776760
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NAME: Patterson, Melinda
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LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                 ADDRESSEE: Arnold, Wh. STREET: P.O. Box 4433
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Matches 1296; Conservative
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ZIP: 77210-4433
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CITY: Houston
STATE: Texas
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                                                     TTTGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAACTCTCGTCTCAGAG
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REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBIL30 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
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                                                                                                                                                            APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1201.6;
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0; Mismatches
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APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/717,370
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
n Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (recombinant)
                                                                                                               Sequence 6, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Hoerner, Dennis R., Jr. REGISTRATION UNBER: 30,514
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
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IBM PC compatible
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95.48;
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Matches 1237; Conservative
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STRANDEDNESS: double
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STATE: Missouri
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US-08-391-339-6
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                                                                                         Plants
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1201.6;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
              6, Application US/08484274A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-6
                                                         APPLICANT: Kishore, Ganesh M. APPLICANT: Barry, Gerard F. TITLE OF INVENTION: Glyphosate NUMBER OF SEQUENCES: 33
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                                                                                                                                                                                                                                                                                                                                                                                     NAME: Patterson, Melinda L. REGISTRATION NUMBER: 33,062
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                                                                                                                                      E: Arnold, White P.O. Box 4433
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LENGTH: 1296 base pairs
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Matches 1237; Conservative
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STRANDEDNESS: double
                                           GENERAL INFORMATION:
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                                                                                                                                                                    Houston
                                                                                                                                                                                 STATE: Texas
COUNTRY: USA
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US-08-484-274A-6
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Patent No.
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                CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGCGGAGGTTGGGGAACTG
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
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REFERENCE/DOCKET NUMBER: MOBIL30 38-21(13560)A
THE LECOMMUNICATION INFORMATION:
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                                                                                                                                 <u>,</u>
                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92.3%; Score 1196.8;
95.2%; Pred. No. 0;
iive 0; Mismatches
                                                                                                                                                         APPLICATION NUMBER: US/08/484,274A FILING DATE: 07 June 1996 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: PATHERSON, MELLAGA L. REGISTRATION NUMBER: 33,062
                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                          TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 3:
                                                                                disk
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LENGTH: 1692 base pairs
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Best Local Similarity 95.2
Matches 1234; Conservative
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                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
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                                                      GTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACC
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OPERATING SYSTEM: PC-00S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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Patent No. 5463175
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                     Score 1160.8;
Pred. No. 0;
0; Mismatches
                                                                                                              NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 4:
FILING DATE:
CLASSIFICATION: 800
PLOR APPLICATION DATA:
PAPPLICATION NUMBER: US/08/156,968
                                                                     APPLICATION NUMBER: US/07/717,370 FILING DATE:
                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
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95.0%;
                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                1293 base pairs
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Best Local Similarity 95.0
Matches 1231; Conservative
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; LOCATION: 1...
US-08-391-339-4
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                                                       FILING DATE:
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, NAME/KEY:
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US-08-484-274A-4
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                                           ACTAACGGTGTTCTCGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACCTCTAAATCA
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas COUNTRY: USA 2.IP: 77210-4433 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-POS/MS-DOS
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CURRENT APPLICATION DATA:
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         38-21(13560)A
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Pred. No. 0;
0; Mismatches
33,062
SR: MOBT130
      REFERENCE/DOCKET NUMBER: MOBT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 789-2679
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                      89.6%;
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Matches 1231; Conservative
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REGISTRATION NUMBER:
                                                                     nucleic acid
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GCGACACCTATGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACA
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                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
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ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kishore, Ganesh M.
PSPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
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FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5463175
GENERAL INFORMATION:
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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0; Mismatches
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                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                       Query Match 89.6%;
Best Local Similarity 95.0%;
Matches 1231; Conservative
(314)537-6099
                                              LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                     GCGACACCTATGGAAATGGGTCTTCGTGTTGCTGGTACTGTTGAGTTTGCTGGTCTCACA
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COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                             ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1412
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ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
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APPLICATION NUMBER: US/08/391,33
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RECISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
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US-08-391-339-8
; Scquence 8, Application US/08391339
; Patent No. 5463175
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ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Missouri
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STRANDEDNESS:
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                                                            Length 1296;
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                                                            DB 1;
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                                                         Score 1011.2;
Pred. No. 0;
0; Mismatches
 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-8
                                                         Ouery Match
Best Local Similarity 86.3%;
Matches 1118; Conservative
linear
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                                         ATTCCTGATTCTCTTCCAGTGATTGGTCGTGCAACTCGTACACCCGACGTAATCTATGCT
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO: 8:
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0; Mismatches 178;
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APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08484274A Patent No. 5776760
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NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
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86.3%;
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MEDIUM TYPE: Floppy disk
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LENGTH: 1296 base pairs
TYPE: nucleic acid
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Best Local Similarity 86.3
Matches 1118; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
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STATE: Texas
COUNTRY: USA
ZIP: 77210-4433
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                            GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTCGTCCTTATGTCC
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1 ATGGCTGAGAACCACAAAAAGTAGGCATCGCTGGAGCTGGAATCGTTGGTGTATGCACT 60
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                                               CTCCTCGCAGGCGAAAAGACCTCAATCGACATTTCGCCCTTTCGCACCAAACCGCTTTGGT
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86.0%; Pred. No. 4.8e-300;
1ve 0; Mismatches 181; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                          Plants
                                                                                                         1261 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
                                                                                                                                                                                                                                                                      ADDRESSE: Dennis R. Hoerner, Jr.,
ADDRESSE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Hoerner, Dennis R., Jr.
RECISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHIONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              Sequence 17, Application US/08391339 Patent No. 5463175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                               ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
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US-08-391-339-17
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Best Local Simi
Matches 1115;
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US-08-391-339-17
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FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REGISTRATION NUMBER: 33,062
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (713)789-2679
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                            COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77.7%; Score 1006.4; DB 2;
86.0%; Pred. No. 4.8e-300;
iive 0; Mismatches 181;
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                                                       1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                           1261 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1296
                                                                                                                                                         APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant INUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                   6 Durkee
                                                                                                                        Sequence 17, Application US/08484274A Patent No. 5776760 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                                                                 ADDRESSEE: Arnold, White STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
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Best Local Similarity 86.0
Matches 1115; Conservative
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STRANDEDNESS: double
TOPOLOGY: linear
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           AGACCAAACAAGGTGAAGGAGCAGGCGAAAGCACTCCGCAATCTCATCAAGTCCACGGTG
                                                          CATCTGACCGTATATCGTGGAGAAGCAGACTTCGCCAAGGACCGGGGGGGTTGGGAACTG
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1128 CGTAATCTATGCTTTTGGTCACGGTCATCTCGGTATGACAGGTGCTCCAATGACTGCAAC 1187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTY: USA
ZIP: 77210-4433
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC.DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/484,274A
FILING DATE: O7 June 1996
CLASSIFICATION: 435
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Patent No. 5776760

GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
TITLE OF INVEWTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Afrold, White & Durkee
STREET: P.O. Box 4433
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38-21(10533)
                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PRIOR DATE:
FILING DATE:
APPLICATION NUMBER: US/07/717,370
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/391,339 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314,537-6099
INFORMATION FOR SEQ ID NO: 33:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (synthetic)
US-08-391-339-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
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                     CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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STATE: Texas
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100.0%; Pred. No. 2.5e-12;
tive 0; Mismatches 0; Indels
                                                    Sequence 30, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
APPLICANT: Rishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 33, Application US/08391339;
Patent No. 5463175;
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.;
TITLE OF INVENTION: Glyphosate Tolerant Plants;
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
                                                                                                                                                                                                                                                                                                                                                                            ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38-21(10533)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: HOEFIEL, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/OOCKET NUMBER: 38-21(1
TELECHONEI (314)537-6099
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERRSTICS:
SEQUENCE CHARACTERRSTICS:
TYPE: nucleic acid
STRANDEDNESS: single
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                                          US-08-391-339-30
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(without alignments)
2407.829 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                          7189864 seqs, 3091403243 residues
                                                     January 1, 2001, 01:12:46
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Maximum Match 100%
Listing first 45 summaries
                                  OM nucleic - nucleic search, using sw model
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em_estfun:*
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Maximum DB seq length: 200000000
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1296
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gb_est39:*
gb_est40:*
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Perfect score:
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117: gb_gss18:*
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119: gb_gss13:*
120: gb_gss21:*
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123: gb_gss22:*
124: gb_gss23:*
124: gb_gss24:*
125: em_gss14:*
126: em_gss16:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AL160534 Lei	904 T	L050434	54 F	A1089448 LX94DII.X	າ ຫ	198 xq13f06	γZ	9 .	8 Drosop	A1350691 QQU48U8.X	C13125 C13125 Yu1i		80	AA250789 zs06a01.s		AA018833 SWUV3MCA1 AI388163 GH18971.5	AI551096 vx37a04.x	F.rubrip	~ <	ALOU4939 F. Fubripe	_ ~	00	9	AI402856 GH22177.5	6 AU0392	g07502r	h01502m	0 AU05293	# œ	0079 7b48d09	35 RPCI-2	q173c08.	tc41903	AW780448 hn92g08.x	1425 0025401	023911 AU023911
SUMMARIES	DB ID	124 P14	123 CNS03	121 CNS000	124 FR000	1.2 A100944	8 AI069309	22 AW4731	38 N50018	34 BE253678	121 CNS015	34	36	123	124	۱ ۲	nп	10	11 A	124	19 AV595356	35		34	10	20	12	-	1 AA065286	7 -	13 AI81441	36	115 AZ1046	9 AI274848	10 A13/9//	24 AW780448 8 AT012527	10 AT33442	14 AU0239
æ	Query core Match Length	1.2 3.2 434	40 3.1	9.2 3.0 1	8.2	2.2 4.7	7.4 2.9	.2 2.9	.8 2.8	.8	20.0	9.0	2.8	.4 2.8	.4 2.8 1	2.8	4. C		36 2.8	5.8 2.8	5.8	2.0	5.6 2.7	5.2 2.7	5.2 2.7	35 2.7	5 2.7	5 2.7	2.7		2.7	5 2.7	5 2.7	2.7	7.7	·. r	2.7	5 2.7
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraadontiformes; Tetraadontoidei; Tetraadontidae; Tetraodon. 1 (bases 1 to 970) (
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 970)
boost-Crollius, H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
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AL050434
                                                                                                                                                                                                                                    Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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/db_xref="taxon:99883"
/clone="026011"
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Pred. No. (
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Best Local Similarity 45.0%;
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COMMENT
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AUTHORS
                                                                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                                                                             Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence Unpublished
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AL243904
GS-424304.
GS-5 genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
                                                                                                                                          2 (bases 1 to 805)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.
Bernot, A., Flzames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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Tetraodon nigroviridis genome survey sequence T7 end of clone
026011 of library G from Tetraodon nigroviridis, genomic survey
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         Bernot, A. and
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                                                            Charaterization and repeat analysis of the compact genome freshwater pufferfish Tetraodon nigroviridis
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Pred. No. 0.28;
0; Mismatches 191; Indels 0;
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   Billault, A., Quetier, F., Saurin, W.,
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/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="005C20"
/clone_lib="H"
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                                                                                                                                                                                                                                            Determination of this PAC-end sequence was carried out as part of a collaboration with the Berkeley prosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on by sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                      part of a
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                                                                                                                                                               Genoscope.

Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
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Eukaryota: Metazoa: Chordata: Vertebrata: Actinopterygii:
Eukaryota: Metazoa: Chordata: Vertebrata: Actinopterygii:
Neopterygii: Teleostei: Euteleostei: Acanthopterygii: Percomorpha:
Tetraodontiformes: Tetraodontoidei: Tetraodontidae: Fugu.
1 (bases 1 to 619)
Elgar.O. Clark.M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams.G. and Brenner,S.
Direct Submission
Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource
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                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR01D09"
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Best Local 77; Conservative
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R., Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center follone distribution: NCI-GGAP clone distribution in NGI-GGAP clone distribution in Section Cound through the I.M.A.G.E. Consortium/LNL at:

Insert Length: 210 Std Error: 0.00

Seq primer: -40UP from Glaco

High quality sequence stop: 407.
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Centre Hinxton, Cambridge, CB10 1SB. Email: blohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
V_type: phagemid
PRIMER: KS
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tx94b11.x1 NCI_CGAP_Ut4 Homo sapiens CDNA clone IMAGE:2277213 3',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 477)
NCI-CGAP http://www.ncbl.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     684 TGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACCACTAACGGTGTTCTGGCTGTTGA 743
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                                                                                                                                                                 One pass dye-terminator sequencing of cosmid cloned genomic
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                                                                                                                                                                                                                                                                                                                                                                                                           103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 124;
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                                                                                                                                                                                                                                                                            /organism="Fugu rubripes"
/db_xref="taxon:31033"
/clone_lib="cosmid 133B16"
/clone="133B16ac7"
/ lone="135 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 38.2;
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                        116 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI689448.1 GI:4900742
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Best Local Similarity 45.5%;
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Gaps

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3'); double-stranded CDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pr773 vector. Library constructed by Bob Barstead. The C2C12 cell line (available from ATCC, catalog # CRL-1772) differentiates rapidly, forming contractile myotubes and producing characteristic muscle proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chol.W., Fang, E., Sasinowski, W., Wing, R. and Dean, R.A. Expressed sequence characterization during appressorium formation in rice blast fungus, Magnaporthe grisea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Germinated conidia on appressorium-inductive surface"
                                                                        A1069309 946 bp mRNA EST 09-DEC-1999 mgae0006cC09f Magnaporthe grisea Appressorium Stage cDNA Library Pyricularia grisea cDNA clone mgae0006cC09f 5', mRNA sequence.
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/clone="mgae0006cc09f"
/clone_llb="Magnaporthe grisea Appressorium Stage cDNA
Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  649 GGTGGCGAATTTGTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAA 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 194 GCTGTCGCTGTTGCTGCTGTTGCCGTAGCATCTGCTGCTGCTGCTGCTGTTGCTGTGCAA 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1989)
Contact: Dean,R.A.
Clemson University Genomics Institute
Clemson University
Clemson University
Tol Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 5737
Fax: 864 656 6793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyricularia grisea.
Pyricularia grisea
Eukaryota; Fungi, Ascomycota; Ascomycota incertae sedis;
Magnaporthaceae; anamorphic Magnaporthaceae; Pyricularia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 2.9%; Score 37.4; DB 6; Length 576; Best Local Similarity 57.1%; Pred. No. 2.1; Matches 68; Conservative 0; Mismatches 51; Indels
    /clone_11b="Barstead mouse myotubes MPLRB5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rdcan@clemson.edu
Seq primer: T3 primer (AATTAACCCTCACTAAAGGG)
High quality sequence stop: 403.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       137 g
                             /cell_line="C2C12
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="70-15"
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                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone='InhaGE:2777213"
/clone=lib="NCI_CGAP_Ut4"
/tissue_type="serous papillary carcinoma, high grade, 2
pooled tumors"
/lab_host="PH108"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT.
Average Insert size 1.48 kb. Life Technologies catalog #:
11542-016"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA754683 576 bp mRNA EST 21-JAN-1998 vu20e10.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1181226 5' similar to gb:M16362 Mouse opa repeat mRNA, 3' end (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 576)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     507 GAICCTCTCTGCTGATGCTTTTGCGTGATTTCGATCCTAACTTGTCGCATGCTTTTACCAA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 GCCTCATTTTCCTGAGGCTCTTCGGGTTTGCTTGCTCATTGGCCGCTGTGTTCATCCAA 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 AGACTICGCCAAGGACCGCGGAGGTIGGGAACTGCGGCGTCTCAACGGTGTTCGCACGCA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      315 ACCCTGGGCAGGGGTGGTACCAGAATGCTGCCTTCCCCCAAGCCTGCCCTCT 256
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Contact: Marra MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 GGGCATTCTTATAGAAGAGAACGGTCACACGATTAATCCGCAAGGGCTCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 12; Length 477;
Pred. No. 1.3;
0; Mismatches 85; Indels
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Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 466.
Location/Qualifiers
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/strain="C3H"
/db_xref="taxon:10090"
/clone="IMAGE:1181226"
Location/Qualifiers
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AA754683.1 GI:2801881
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1 Similarity 51.1%;
89; Conservative (
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Matches 89; Conserv
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14-FEB-1996

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yzl0a01.sl Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA
clone IMAGE:282600 3' similar to contains element MER22 repetitive
element ;, mRNA sequence.
742 GATGCAGCTGTTGCAGCTGGTGCACACTCTAAATC 779
                    137 ACTGACGCTGTTATTGGAACTGGTACTGGCACAAGAGC 174
                                                                                                                                      mRNA
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                                                                                                                                      554 bp
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Best Local Si
Matches 62,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
Tal: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
Found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 226)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                 AW473198 226 bp mRNA EST 24-FEB-2000 xq13f06.x2 NCI_CGAP_Utl Homo sapiens cDNA clone IMAGE:2750531 3' similar to TR:076058 076058 DJ1409.2;, mRNA sequence.
                                                                                                                                649 GGTGGCGAATTTGTATCTGCGCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTAAA 708
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                                                                                                                                                                                                              709 GGCATTACAACCACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGC 767
                                                                                                                                                                                                                                  Trace considered overall poor quality
Seq primer: -400P from Gibco
High quality sequence stop: 1.
Location="Valuation" Homo saplens"
(Acronism="Homo saplens"
/Ab_xre="tamon:9606"
/Clone="IMAGE:2750531"
/Clone="IMAGE:2750531"
/Clone="IMAGE:Appe="Well-differentiated endometrial adenocarcinoma, 7 pooled tumors"
//Lab_host="PH108"
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                                                     DB 8; Length 946;
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51.2%; Pred. No. 1.8;
Ive 0; Mismatches 38;
                                                     Score 37.4; DE Pred. No. 2.5; 0; Mismatches
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                                                   Query Match 2.9%;
Best Local Similarity 57.1%;
Matches 68; Conservative
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Unpublished (1997)
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Best Local Similarity
Matches 60; Conserv
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
COMMENT
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KEYWORDS
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FEATURES

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fortaccartreaagreegeacececartrtrtrtrtrtrtrtrtr 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pr7r3 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis
lesions from one patient was kindly provided by Dr. Kevin
G. Becker (NINDS/NIH).
a 153 c 141 g 111 t 7 others
                                                                The bases I to 554)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Kullaman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R., Green, M., Tan, F., Trevaskis, E., Waterston, The Washu-Merck EST Project
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parky, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Seq primer: mil 3-40 forward
High quality sequence stop: 381.
Location/Qualifiers
1. .554
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/db_xref="temp:"spills"
/db_xref="temp:"spills"
/db_xref="temp:"spills"
/db_xref="temp:"spills"
/db_xref="temp:"spills"
/db_xref="temp:"spills"
/clone="IMAGE:282600"
/clone="IMAGE:282600"
/clone="image:282600"
/clone="image:282600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="bill0B (ampicillin resistant)"
/note="Vector: pr773D (Pharmacia) with a modified
polylinker v_TYPE: phagemid; Site_1: Not I: Site_2: Ec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               669 GCGTGTCATCGGTTTTGAGACTGAAGGTCGTGCTCTCAAAGGCATTACAACCACTAACGG 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292 GCGTGTTAGGGCTGGATCCGGCCATGGTCTGGCTCAAAGCNTNTTTCCGCCCGCNTGCCC 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                729 TGTTCTGGCTGTTGATGCAGCTGTTGCAGCTGGTGCACACTCTA 775
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RESULT 11 BE253678/c

g

DEFINITION

ACCESSION VERSION KEYWORDS ORGANISM

SOURCE

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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A1350691 377 bp mRNA EST 13-FEB-1999 qq04a08.x1 Soares_NHHMPu_S1 Homo sapiens cDNA clone IMAGE:1931510 3' similar to contains element MER22 repetitive element ;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  113 CTCCTGGCGAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCCGTCGTC 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          173 CTATGTCCATGCCGGGAAACTTGACGAGCGTGCCGAAGTGGCTCCTTGACCCGATGGGGC 232
                                                            fruit fly.
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorphia; Ephydroidea; Drosophilldae; Drosophila.

1 (bases 1 to 922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                233 CGTTGTCAATCCGGTTCAGCTATTTTCCAACCATGATGCCTGGTTGATTCGCTTTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .922
/organism="brosophila melanogaster"
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="brosbAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="BACN15P08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="end : SP6"
147 c 154
                        GI:5619823
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AI350691.1 GI:4087897
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Unpublished (1997)
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  AL106058
AL106058.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            pBeloBAC11
                                                                                                                                                                                              Genoscope.
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ORGANISM
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                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                 AUTHORS
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                                               KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/dbexref="taxon:9606"
/clone="InAGE:3351490"
/clone="InAGE:3351490"
/clone="Lib="NIH_AGC.16"
/tissue_type="retinoblastoma"
/tab.host="Dh108 (phage-resistant)"
/note="Organ: eye; Vector: pOTBT; Site_1: XhoI; Site_2: EcoRI: cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAGGG). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of an the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                           BE253678 816 bp mRNA EST 13-JUL-2000 601110742F1 NIH_MGC_16 Homo sapiens CDNA clone IMAGE:3351490 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM149 row: c column: 11
High quality sequence stop: 719.
Location/Qualifiers
1. 816
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 AGCGCGGACTGCGTCGGGCACGGGCTGAGGCGTGTTAGGGCTGGATCCGGCCATGGTCTG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   700 GCTCTCAAAGGCATTACAACCACTAACGGTGTTCTGGCTGTTGATGCAGCTGTTGTTGCA 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 816)
NIH MGC http://www.ncbl.nlm.nih.gov/MGC/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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232 TGTCCGGGCTGTTGATGCTGCTGCTGCTGCTGCTGCTGCTCCCACCA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
2.8%; Score 36.8; DR
Best Local Similarity 54.4%; Pred. No. 3.6;
Matches 74; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. 18-1: (301) 496-1550 Email: Robert_Strausberg@nih.gov Tissue Procurement: ATCC
                                                                                                                                                                                          BE253678.1 GI:9124097
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                                                                                                                                                  mRNA sequence.
BE253678
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source

FEATURES

BASE COUNT ORIGIN

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Caps

292

RESULT 12 CNS015Y8/c LOCUS DEFINITION

166

FEATURES

COMMENT

us-08-484-274-7.rst

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/clone_lb="Gm-close" conc. Do. on the cotyledons"
/lab_host="whole seedling without cotyledons"
/lab_host="bluescriptii SK+; Site_l: EcoRi; Site_2:
/note="Vector: pBluescriptii SK+; Site_l: EcoRi; Site_2:
Xhoi; This cDNA library was constructed from mRNA isolated
from 2 week old seedlings with the cotyledons removed at
the time of harvest. The seedlings for the cultivar Ogden
were grown in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a Xhoi restriction
site. EcoRi adapters were ligated to the blunt-ended cDNA
fragments followed by Xhoi digestion. The cDNA fragments
were directionally cloned into the EcoRi-Xhoi restriction
site of the pBluescript vector. The ligated cDNA fragments
were transformed into DH10B host cells (Gibco BRL). This
library was constructed by Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditodea
Rhabditidae; Peloderinae; Caenorhabditis.
(bases 1 to 353)
Koharayr., Motohashi,T., Tabara,H., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A. and Nishigaki,A.
Expression map of the C.elegans genome
                                                                 This clone is available through: Genome Systems, Inc. 4633 World Barkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com High quality sequence stop: 411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C13125 153 bp mRNA EST 28-DEC-1998 C13125 Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA clone ykl64d4 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                689 CTGAAGGTCGTGCTCTCAAAGGCATTACAACCACTAACGGTGTTCTGGCTGTTGATGCAG 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 CTAAAGATAAAGTTATGGAGGCAATTAAAACTATGAAAGATGATCTGGAGAATGATGATA
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                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1039-1370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 36.6; DB 34; Length 521;
Pred. No. 3.5;
0; Mismatches 49; Indels 0:
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Tel: 81-559-81-6854
Fax: 81-559-81-6855
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/organism-"Glycine max"
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Contact: Yull Kohara
Gene Library Lab
National Institute of Genetics
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Location/Qualifiers
                                        Email: est@watson.wustl.edu
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/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I: Site_2: Eco RI: Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbH10, and fetal heart NbH110H) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries: The pools consisted of I.M.A.G.E. clones 260232-265223,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Bukaryotta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Pabaleas; Pabaceae; Papilionoideae; Glycine.

Fabaleas; Fabaceae; Papilionoideae; Glycine.

I (bases 1 to 521)

Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Warrah, W., Hillier, L., Kucaba, F., Martin, J., Beck, C., Wylle, T., Underwood, K., Steptoe, M., Pape, D., Harvey, N., Schurk, K., R., Ritter, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.,

Unpublished (1999)

Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BEZ10590 521 bp mRNA EST 29-JUN-2000 so50d01.yl Gm-c1039 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1039-1370 5' similar to TR:O64760 O64760 PUTATIVE TRANSLATION BEZ10590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 860 Std Error: 0.00
Seq primer: -40UP from Glbco
Seq primer: -40UP from Glbco
Location/Qualifiers
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                                                                                                                                                                                                                                               0; Gaps
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115 a 76 c 78 9 76 t 8 others
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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928.8 71.7 1689 5 I15324 66.2 5.1 3430 2 PSEAKSD 58.8 4.5 62 5 AR016615 58.4 4.5 69 5 AR016616 58.4 4.5 69 5 AR016616 58.4 4.3 69 5 AR016618 56.2 4.3 69 5 AR016618 56.2 4.3 69 5 AR016618 53.6 4.1 68 5 AR016617 57.8 4.1 68 5 AR016617 50.3 9 2289 2 PSEKSDA 49.4 3.8 7218 5 I65494 49.4 3.8 7218 5 I65494 49.4 3.8 7218 5 I66494 40.4 3.6 179553 49 AC073755 46.4 3.6 179553 49 AC073755 47.6 3.5 186935 48 AC072322 44.8 3.5 31206 bp DNA AR016595 1 GI:3972872 AR016796 1 GI:3972872	115324 Sequence 3 M09158 Pseudomonas AR016613 Sequence 115346 Sequence 27 AR016616 Sequence 115349 Sequence 115352 Sequence 115352 Sequence 115351 Sequence 115351 Sequence 115351 Sequence 115351 Sequence 115351 Sequence 115351 Sequence 115350 Sequence 115350 Sequence 115350 Sequence 115350 Sequence	115347 Sequence 28		aps 60 60 120 120
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Db 601 AACCCACAAGGTCTCGTGACTCTTGTTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC 660 Qy 661 GTGTCTGCTGTTATCGGATTCGAGCTGAAGGTCGTCTCCAAGGGTATCACCACC 720 Db 661 GTGTCTGTTATCGAATTCGAAGTTGAAGGTCTTCTAAGGGTATCACCACC 720	721 ACCARGGGGTGTTGTGGGGGTGTTGGGGGGGTGTGGGGGGGGG	QY 1021 GCTCTCGCTCCTGCCAGTTCTGAAGACGTTACTCCAAGTGGATGGGTTCCGTCCAAGC 1080 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 3 AR016604 LOCUE	Query Match 99.4%; Score 1288; DB 5; Length 1296; Best Local Similarity 99.6%; Pred. No. 0; Matches 1291; Conservative 0; Mismatches 5; Indels 0; Gaps
Oy 1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296 	15328	Query Match 100.0%; Score 1296; DB 5; Length 1296; Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 ATGGCTGAGACCACAAGAAGTTGGTATCGTGGAATCGTTGGTGTTTGCACT 60 111111111111111111111111111111111111	Qy 241 ATCGGTTCAGCTACTTCCAACCATCATGGTTGTTCTTGCTTG	Qy 541 CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATGGAAGAGAACGGTCACACCATC 600 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

Db 1081 Qy 1141 Db 1141 Oy 1201 Db 1201 Oy 1261	RESULT 4 115337 1000S 1000S DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUICG BASE COUNT	Ouery Matc Best Local Matches I AI Qy I AI Db I AI	9y 61 Db 61 Qy 121 Db 121		0,0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 17 31-OCT-1995;
Location/Qualifiers
1. 1296
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FEATURES Location/Qualifiers source 1. 1631 /organism="Arabidopsis sp." /db_xref="taxon:29726" BASE COUNT 342 a 454 c 381 g 454 t ORIGIN	Query Match Best Local Similarity 95.3%; Pred, No. 0; Matches 1283; Conservative Matches 13: Indels 50: Gans 2	TEGETGAGAACCACAAGAAGGTTGGTATCGTGGAGCTGGAATCGTTGGTGTTTGCACT 60	GCTTTGATGCTTCAACGTCGTGGATTCAAGGTTACCTTGATTGA	Qy 121 GAAGGTGCTTCTTTCCGTAACGCTTGCTTTGCTTCCACGGTTCCTCCGTTGTTCCAATGTCC 180	181 ATGCCAGGAAACTTGACTAGGGTTCCAAAGTGCTTCTTGACCAGTTCCTTCATCAGTTCCAAAGTGCTTCTTGACTAGTGTTCAAAAGTGCTTCTTGACTAGAAAGTGCTTCAAAAGTGCAAAGTGCAAAGTGCAAAAAGTGCAAAAAAAA	224CAPTGGGTCCATTGTCCATCGTTTCAGGTACTTTCCAACATCATGCTTG 27 514 TTACGGATCCATGGTCCATCGTTTTCAGCTACTTTCCAACATCATGCTTG 57		336 CGGTAACCTCATCAGTCCACTGTGCTTGATCAAGTCCTTGGCTGAGGGCTGATGC 39 [396 TAGCCACCTTATCGTCACGTCACGAGGTCACCGTTACCGTGACGAGAAGCACTTGG 45 11111111111111111111111111111111111	CAAGGACCGTGGAGGTTGGGAACTTCGTCGTCTCAACGGTGTTCGTACTCAAATCCTCAG 51	516 CGCTGATGCATTGCGTTTTCGATCCTAACTTGTCTCACGGTGTTACCAAGGGAATCCT 57 [576 TATCGAAGAACGGTCACACCATCAACCCACAAGGTCTCGTGACTCTCTTGTTTCGTCG 63 11111111111111111111111111111111111	OY 636 TITCATCGCTAACGGTGGAGAGTTCGTGTCTCGTGTTATCGGATTCGAGACTGAAGG 695	Oy 696 TCGTGCTCTCAAGGGTATCACCACCACGAGGTGTTCTTGCTGTTGATG 745	OY 746	QY 791 CCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCCAACC 850 LILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	910
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9y 241 ATCCGTTTCAGCTACTTTCCAACCATCATGCCTTGGTTGATTCTTTCT	09 721 ACCAACGGTGTTGTGCTGTTGTTGCAGCTGTTGCAGCTGGTGCACCTCCAAGTCT 780 721 ACCAACGGTGTTTGTTGATGCAGCTGTTGTTGCAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
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           CTTGCTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTG
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Pred. No. 1.5e-260;
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Barry, G. Francis and Kishore, G. Murthy Glyphosate tolerant plants
Patent: US 5776760-A 6 07-JUL-1998;
Location/Qualifiers
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Pred. No. 1.5e-274;
0; Mismatches 178;
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Barry, G.F. and Klshore, G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 7 31-OCT-1995;
Location/Qualifiers
                            5463175
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344 c 332 g
                Sequence 7 from patent US 54
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86.3%;
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Matches 1118;
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Pred. No. 1.5e-260;
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                                            ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
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Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 3463175-A 6 31-OCT-1995;
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Sequence 6 from patent US 5463175.
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Barry, G. Francis and Kishore, G.Murthy, Glyphosate tolerant plants
Patent: US 57/6760-A 3 07-JUL-1998;
Location/Qualifiers
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1 (bases 1 to 1689)
Barry,G.F. and Kishore,G.M.
Glyphosate tolerant plants
Patent: US 5463175-A 3 31-OCT-1995;
Location/Qualifiers 360 1689 bp DNA 3 from patent US 5463175. 1. .1689 /organism="unknown" δ 468 71.7%; 83.8%; GI:1250232 479 c Best Local Similarity 83.8 Matches 1086; Conservative Unclassified. 115324 Sequence 3 115324 115324.1 ø 381 Unknown Unknown Query Match source DEFINITION ORGANISM BASE COUNT ORIGIN 1018 1021 1081 1078 1138 1201 1198 1.80 121 300 301 868 AUTHORS JOURNAL 61 240 ACCESSION REFERENCE KEYWORDS SOURCE FEATURES TITLE VERSION q q q g QQ qq q ò ò δ á ð á ò ò δ ò ò 3, GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC 180 300 297 360 357 420 417 540 009 597 999 657 720 717 780 CTTGCTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTG 840 GCTACTCCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT 960 9 ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC ATCCGTTTCACCTACTTTCCAACCATCATGCCTTGGTTGATTCGTTTCTTTGCTGGA AGACCAAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG CGTCGTCTCAACGGTGTTCGTACTCAAATCCTCAGCGCTGATGCATTGCGATTTCGAT CTTGCTAATTCGCTAGGCGATGACATCCCGCTCGATACCGAACGTGGATATCATATCGTC ATCGCCAACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATC ATGGCTGAGAACCACAAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTTGCACT CCTTTGATCAAGTCCTTGGCTGAGGCTGATGCTAGCCACCTTATCCGTCACGAAGGT CCTAACTIGICICACGCCTITACCAAGGGAATCCTIATCGAAGAGAACGGTCACATC **AACCCACAAGGTCTCGTGACTCTTGTTTTCGTCGTTTCATCGCTAACGGTGGAGAGTTC** GTGTCTGCTCGTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACCACC ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACCTCCAAGTCT 3, Length Indels Score 928.8; DB 5; Pred. No. 2.8e-251; 0; Mismatches 207; Ļ 281 Location/Qualifiers 1. .1293 /organism="unknown" 367 c 359 g б 71.7%; 83.8%; Conservative Similarity Query Match Best Local Simi Matches 1086; COUNT 61 121 181 241 240 301 358 478 538 601 298 661 658 721 121 181 298 361 121 418 181 541 781 778 901 FEATURES ORIGIN BASE a g a g g g g ð qq ò 8 ò ò Q ò ò 8 õ ò ò g ò ò g ò g ô ò ò a ò

3 1140 1200 1017 1077 957 179 120 239 180 299 240 358 300 416 AGACCAAACAAGGTGAAGGAGCAAGCTAAGGCACTCCGTAACCTCATCAAGTCCACTGTG 360 Gaps 9 02-APR-1996 GCGACACCTATGGAAATGGGGCTTCGCGTGGCGGGTACGGTTGAGTTCGCTGGGCTCACA ATCCCAGATTCCCTTCCAGTGATTGGTCGTGCTACCCGTACTCCAGACGTTATCTACGCT 1141 TTCGGTCACGTCACCTCGGTATGACTGGTGCTCCAATGACCGCAACCCTCGTTTCTGAG 1 ATGCCTGAGAACCACAAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTTGCACT GAAGGTGCTTCTTTCGGTAACGCTGGTTGCTTCAACGGTTCCTCCGTTGTTCCAATGTCC GAAGGTGCATCGTTTGGGAATGCCGGATGCTTCAACGGCTCATCTGTCCTTTGTCC 181 ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC GCTGCTCCTAACTGGAAGCGTGCTCACGTTCTTCTACACTCACGCTCGTAAGTTGCTTTCCA GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCCGTCCAAGC CTCCTCGCAGGTGAGAAGACCTCTATCGACATCTCTCCATTCGCACCAAACCGTTTCGGT 3; Length 1689 others Indels -Score 928.8; DB 5; Pred. No. 2.8e-251; 0; Mismatches 207; ı

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PSEAKSD 3430 bp DNA BCT 26-APR-1993 Pseudomonas putida alpha-ketoglutarate semialdehyde dehydrogenase gene, complete cds.

LOCUS

RESULT 14

PSEAKSD

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Burlingame, R.P., Maruya, A., Ally, A.H., Ally, D. and Backman, K.C.
Nucleotide sequences of hydroxyproline-specific alpha-ketoglutarate
semialdehyde dehydrogenase genes from two strains of pseudomonas
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TITLE
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4.5%; Score 58.8; DB 5; Length 62;
Best Local Similarity 96.8%; Pred. No. 1.4e-05;
Matches 60; Conservative 0; Mismatches 2; Indels
                           PAT
                                                                                     Unknown.

Winknown.
Unclassified.

E 1 (bases 1 to 62)
S Barry, G.Francis and Kishore, G.Murthy.
Glyphosate tolerant plants
AL Patent: US 5776760-A 27 07-JUL-1998;
Location/Qualifiers
1.62 "...nknown" 19 t
                        AR016613 62 bp DNA
Sequence 27 from patent US 5776760.
AR016613.1 GI:3972890
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Unknown.
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RESULT 15
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GenCore version ght (c) 1993 - 2000 rch, using sw model	January 1, 2001, 03:43:13 ;	US-08-484-274-8 1296 1 ATGGCTGAGAACCACAAGAA	IDENTITY_NUC Gapext 1.0	480022 seqs, 187831343 residues	hits satisfying chosen parameters	length: 0 length: 2000000000	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	N_Geneseq_36:* 1: /SIDS6/gegdata/geneseq/ges 2: /SIDS6/gegdata/geneseq/ges 3: /SIDS6/gegdata/geneseq/ges	/ Stubs/Aggdacugeneseq/geneseqn/NAL983.DAT:* 5: /SIDS6/aggdacua/geneseq/geneseqn/NAL984.DAT:* 6: /SIDS6/aggdacua/geneseqn/NAL985.DAT:* 7: /SIDS6/aggdacua/geneseqn/NAL985.DAT:* 7: /SIDS6/aggdacua/geneseqn/NAL985.DAT:* 7: /SIDS6/aggdacua/geneseqn/NAL986.DAT:*	s: /sibso/gcgdata/geneseq/ge 3: /sibs6/gcgdata/geneseq/ge \0: /sibs6/gcgdata/geneseq/g	11: /SIDS6/gcgdata/geneseq/g 12: /SIDS6/gcgdata/geneseq/g	13: /SIDS6/gcgdata/geneseq/g	15: /SIDS6/gcgdata/geneseq/g \6: /SIDS6/gcgdata/geneseq/g	17: /SIDS6/gcgdata/geneseq/g 18: /SIDS6/gcgdata/geneseq/g	19: /SIDS6/gcgdata/geneseq/geneseqn/Na1998.DAT:* 20: /SIDS6/gcgdata/geneseq/geneseqn/Na1999.DAT:*	1: /sibsb/gcgdata/geneseq/g	than or equal to the	SUMMARIES	Query Match Length DB ID	1296 13	8418 20 1631 18 1321 13	1321 13	1689 13	69.2 8798 20 X57308 3.1 32207 20 V73805	397 20
ucleic -	Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of h	Minimum DB seq le Maximum DB seq le	Post-processing:	Database :		- 5. 11			r. cl			o N	is.		Result Score N	1 1296	1296 1205.2	956.8	925.6 897	9 897 10 39.8	37.4

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                                                  The sequence is that of the gene encoding a glyphosate oxidoreductase (GON) enzyme, the gene sequence was synthesised so that it could be redesigned to eliminate as much as possible the following sequences or redesigned to eliminate as much as possible the following sequences or sequence features (while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of 5 or more; A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + C% for the synthetic gene is 51% and the potential to form short, high energy, hair-pin structures is reduced. However it still encodes the wild type GOR enzyme. It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant.

Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops.
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 to produce plants tolerant to glyphosate
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Pred. No. 0;
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Best Local Similarity 100.
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herbicide;
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                                                                                                                                                                                                                                                                      Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plar
5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herk
tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
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expression cassette; inducible promoter; alch; alch; aldh; regulator; alcohol dehydrogensse; herbicide resistance gene; glyphosate; N-phosphonomethyl-glycine; glyphosate oxidase; GOX; EPSPS; 5-enol-pyruvylshikimate 3-phosphate CP4; chloroplast transit sequence Arabidopsis; RUBISCO; CPT1; dicotyledon; monocotyledon; crop; ss.
ategecaacecagaagetgetecacgtattecaactacegatgettetggaaagtteate
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                                                                    This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capable of tolerating herbicide treatment with glyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
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                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                           8418;
                                                                                                                                                                                                             Sequence 8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 other;
                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                          20;
              beet plants
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                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                        100.0%; Score 1296;
100.0%; Pred. No. 0;
.ive 0; Mismatches
              transgenic sugar
                                           15; Page 36-41; 55pp; English
                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 1296; Conservative
              Glyphosate resistant
                                                                                                                                                                                                                                                           Query Match
                                           Claim
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Tue

873

814 cyctgatgcattgcgtgatttcgatcctaacttgtctcacgcctttaccaagggaatcct

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Inducible promoter linked to a gene (I) that confers resistance to a herbicide, is calaimed. (I) imparts resistance to a herbicide, is calaimed. (I) imparts resistance to N-phosphonomethyl-c glycine (glyphosate) or its salts, but may also be a gene for resistance to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolones, to, e.g. chloroacetanilides, glufosinate, sulphonyl ureas, imidazolones, cetc. The inducible promoter (e.g. alcA, alcR, aldA or other alcR-induced expression of (I) avoids the risk that constitutive expression interfere with plant development; allows volunteer plants to be controlled by herbicide applied without inducer and minimises the chance that herbicide resistant strains of weeds will arise. The expression cassette is strictly controlled and suitable for general use in plants (both mono- and dicotyledons). The alcA/alcR gene switch was used to drive inducible expression of glyphosate oxidase (GOX) in plants. Switchable GOX was expressed alone or in conjunction with constitutive expression of 5-enol-pyruvylshikimate 3-phosphate (BPSPS) CP4. Constructs were optimised for expression in mono- and dicotyledonous crop species. The present sequence comprises a fusion of the GOX gene fused to the chloroplast transit sequence a from Arabidopsis RUBISCO (CPT1). This
     avoids constitutive expression and minimises development
                                                                              Example 3; Fig 7; 59pp; English.
                            herbicide tolerant weeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cot vectors.
     glyphosate,
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Sequence 1631 BP; 342 A; 454 C; 381 G; 454 T; 0 other;

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                        Gaps
                                                       1 ATGGCTGAGAACCACAAGAAGGTTGGTATCGCTGGAGCTGGAATCGTTGGTGTTTGCACT
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                                                                                                                                                                                                                                                                              -----CAATGGGTCCATTGTCCATTCGGTTTCAGCTACTTTCCAACCATCATGCCTTG
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                                                                                                                                                                            ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1631;
                        50;
                        Indels
  DB 18;
                       13;
Score 1205.2;
Pred. No. 0;
0; Mismatches
                                                                                                                                                                                         93.0%;
           Best Local Similarity 95.3
Matches 1283; Conservative
  Query Match
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                                                                                                                        1054 gtgaattcaagcttactgcagttgttgcagctggtgcacactccaagtctcttgctaact
                                                                                                                                                                                                                                           1114 cccttggtgatgacatcccattggataccgaacgtggataccacatcgtgatcgccaacc
                                                                                                                                                                                                                                                                                                                                                                                                                                              TATCGAAGAACGGTCACACCATCAACCACAAGGTCTCGTGACTCTCTTGTTTCGTCG
                          tategaagagaaeggteacaecateaaceeaaaggtetegtgaetettgtttegteg
                                                     TITCATCGCTAACGGTGGAGGTTCGTGTCTGCTCGTGTTATCGGATTCGAGGCTGAAGG
                                                                               934 tttcatcgctaacggtggagagttcgtgtctgctcgtgttatcggattcgagactgaagg
                                                                                                                                                                                                                                                                      851 CAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATGGCTACTCCTA
                                                                                                                                                                                                                                                                                     TGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACTGCTGCTCCTA
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                                                                                                                                                               ------CAGCTGTTGTTGCAGCTGTGCACCTCCAAGTCTCTTGCTAACT
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                                                                    696 TCGTGCTCTCAAGGGTATCACCACCACCGTGTTCTTGCTGTTGATG
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                               CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAAGGACCGTGGAGGTTGGGAACTT
                                                                                              CGTCGTCTCAACGGTGTTCGTACTCAAATCCTCAGCGCTGATGCATTGCGTGATTTCGAT
                                                                                                                                                         CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAGAACGGTCACACCATC
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                                                                                                                                                                                                                                                                                                                                                          The sequence is that of the gene encoding a glyphosate oxidoreductase (GOR) enzyme which has been modified using mutagenic primers. The gene sequence was redesigned to eliminate as much as possible the Gollowing sequences or sequence features (while avoiding the introduction of unnecessary restriction sites), stretches of G's and C's of S or more: A + T rich regions (predominantly) that could function as polyadenylation sites or potential RNA destabilisation regions, and codons not frequently found in plant genes. The G + Cs of the GOR gene was reduced from 56% in the manipulated version (120833) to 52% in the modified version. However it still encodes the wild type GOR enzyme. It was obtd. From bacterial isolate LBAA.

It is used to transform plants such that they express the enzyme sufficiently to enhance the glyphosate tolerance of the plant.

Transformed plants resistant to glyphosate can be obtd. so that weeds can be selectively controlled in fields contg. crops.
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                                                                                                                                                                                                                                                                     Gene encoding glyphosate oxido-reductase enzyme - used to
transform plants to produce plants tolerant to glyphosate
herbicide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1009.6;
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 102; 142pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           see also Q20832-Q20841 and Q22705
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                                                                                                     910S-0717370.
                                                                            91WO-US04514
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                                                                                                                                                                                        Barry GF;
                                                                                                                                                         (MONS ) MONSANTO CO.
                                                                                                                                                                                                                      WPI; 1992-041559/05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                     P-PSDB; R20642
                                                                         24-JUN-1991;
                                                                                                        24-JUN-1991;
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                                                                                                                                                                                       Kishore GM,
             WO9200377-A
                                            09-JAN-1992
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/note= "encodes wild type glyphosate oxidoreductase"
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transform plants to produce plants tolerant to glyphosate
herbicide
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83.8%; Pred. No. 1.2e-285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 210;
                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              English
 Recombinant; GOR; resistance;
                                                                                                                                                                    91WO-US04514
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90US-0543236
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                         isolate LBAA.
                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 3; 142pp;
                                                                                                                                                                                                                                                             Barry GF;
                                                                                                                                                                                                                                                                                    WPI; 1992-041559/05.
P-PSDB; R20642.
                                                                                                                                                                                                                                  (MONS ) MONSANTO CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                    24-JUN-1991;
                                                                                                                                                                                            24-JUN-1991;
25-JUN-1990;
                                                                                                                WO9200377-A
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                                                                                                                          /note= "glyphosate oxidoreductase coding region"
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                                                                                                                                                         /*tag= b
/note= "not present in alternative sequence"
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/note= "not present in alternative sequence"
                                                                                                                                                                                                                                                                           "not present in alternative sequence'
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transform plants to produce plants tolerant to glyphosate
herbicide
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                                                                         Location/Qualiflers
120..1415
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig 2; 142pp; English.
             GOR; resistance;
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/note=
                                            Bacterial isolate LBAA.
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P-PSDB; R22262.
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             Recombinant;
                                                                                                                                             misc_feature
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Best Local Simi
Matches 1084;
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                                                    CACCTTACCGTGTACCGTGGAGAAGCAGACTTCGCCAAGGACCGTGGAGGTTGGGAACTT
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/note= "in the alternative sequence T is |
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/*tag= d
/note= "in the alternative sequence C is |
                                                                                                                                                                                                                                                                                                                                           oxidoreductase coding
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                                                                                                                                                                                                                                                                                                                                                   749..350
/*tag= b
/note= "in the alternative sequence
375..376
1380 attggcaaatccaagcaaacgggtccggcaagttaa 1415
                                                                                                                                                                                                                                                                                         Location/Qualifiers
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/note= "glyphosate
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                                                                                                                                                                                     Glyphosate oxidoreductase gene
                                                                                  BP
                                                                                                                                                                                                                     Recombinant; GOR; resistance;
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90US-0543236
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                                                                                  DNA; 1689
                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                        Bacterial isolate LBAA.
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                                                                                 Q20832 standard;
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GCTCTCGCTCCTGCCAGTTCTGAAGAACGTTACTCCAAGTGGATGGGTTTCCGTCCAAGC

ATCCCAGATTCCCTTCCAGTGATTGGTCGTGCTACCCGTACTCCAGACGTTATCTACGCT

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Gaps 9

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Indels

Length 1689;

DB 13;

Score 925.6; DB 13; Pred. No. 5.4e-275; 0; Mismatches 209;

Query Match
Best Local Similarity 83.6%;
Matches 1084; Conservative

1 ATGCTGAGAACCACAAGAAGGTTGGTATCGCTGGAGGTGGAATCGTTGGTGTTTGCACT

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Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
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                                                             ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC
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                                                                                 This invention describes a novel sugar beet plant, including its descendants expressing 5-enolpyruvishikimate-3-phosphate synthase (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated transformation with a gene allowing expression of cp4/epsps in plants, where the plant lacks both right and left T-DNA border sequences. The transgenic sugar beet plants of the invention are capa of tolerating herbicide treatment with allyphosate (also known as N-phosphonomethyl-glycine) as the active ingredient, e.g. Roundup.
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                                                                                                                                                                                                                                                                                                   Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant; 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide; tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
                       TTCGGTCACGGTCACCTCGGTATGACTGGTGCTCCAATGACCGCAACCCTCGTTTCTGAG
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llarity 100.0%; Pred. No. 7.7e-266;
Conservative 0; Mismatches 0;
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES
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100.0%; Pred. No. 8.1e-266;
ive 0; Mismatches 0;
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                                           ) NOVARTIS AG.
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This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67 which encodes tegument protein IV, ORF68 which encodes a glycoprotein, ORF69, KI2 which encodes immediate early protein (IEP), KI4 which encodes (ORF73 which encodes cyclin D, ORF73 which encodes (Protein Coupled receptor, ORF75 which encodes (ORF73 which encodes (ORF75 which encodes (ORF7
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es virus nucleic acid - encodes useful for treatment, prophylaxis
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Sequence 137507 BP; 32579 A; 37795 C; 35758 G; 31375 T; 0 other;
                     CDS
                                                 CDS
                                                                             CDS
                                                                                                         CDS
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                                                                                                                                                                                                                                                                                                                                                                 KSHV; HHVB; human herpes virus 8; macrophage inflammatory protein II; interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection; immediate early protein; Kaposi's sarcoma; protective vaccine; lymphoma; lymphoprollferative disease; leukaemia; splenomegaly; mycosis fungoides; HIV immune status; anti-inflammatory agent; therapy; ds.
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                                                                                                       787 AACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCC 846
                                                                                                                                                                                  CCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACTGCTGCT 966
                                               0; Gaps
                                                                                                                                            AACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACT
                              Length 32207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product- macrophage inflammatory protein II complement (27137..27424)
Sequence 32207 BP; 7229 A; 9156 C; 8713 G; 7109 T; 0 other;
                                                Indels
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28661..29741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement-binding protein
                                                                                                                                                                                                                                                                                                                                                 KSHV long unique coding region and terminal repeat.
                           Score 39.8; DB 20;
Pred. No. 0.14;
0; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= interleukin 6
complement (21548..21832)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= glycoprotein B complement (17261..17875)
                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaposi's sarcoma-associated herpes virus.
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8699..11236
                            Query Match 3.1%;
Best Local Similarity 47.7%;
Matches 116; Conservative
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/*tag= a
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                                                                                                                                                                                                                                                                                                                             03-AUG-1998 (first entry)
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V19941
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This sequence represents the long unique region and terminal repeat of the Kaposi's sarcoma-associated herpes virus (KSHV). KSHV is also known as human herpes virus 8 (HHWA). This sequence contains the DNAs of the invention which encode KSHV polypeptides selected from: (a) viral complement broad protein; glycoproteins B, Mor L; (c) viral IRF1. (d) complement binding protein; glycoproteins B, Mor L; (d) capsid protein; glycoproteins B, Mor L; (d) capsid protein; lycoproteins B, Mor L; (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the proteins are useful for detecting HHVB, specific for the proteins are useful for detecting HHVB, specifically for diagnosis of Kaposi's sarcoma, in body fluids or tissue samples. HHVB infections can be treated with antisense or triplex forming molecules or agents that bind specifically to the protein. Ab may be used for prophylaxis or treatment of HHVB infection, while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHVB may be implicated in many other lymphoproliferative diseases such as lymphomas, leukaemia, containing the concentrative diseases such as lymphomas, leukaemia, splenomegaly and mycosis fungoides. Cells and animals containing the cused as targets for antiviral drugs, e.g. dihydrofolate reductase gene can be inhibited with methotrexate. These can also be used to determine the immune status of a patient infected with HTV HHVB derived protein propertion and an animal for the immune status of a patient infected with HTV HHVB derived protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral MIP III may be used as an anti-inflammatory agent for, e.g. treating rheumatoid arthritis. This sequence is stated as containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid encoding Kaposi's sarcoma associated herpes virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins – useful for, e.g. detecting levels of HHVB in, and preparation of vaccines for treatment of, HIV patients
                                                                 /product interferon regulatory factor 3 90173..90643 /*tag k
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   interferon regulatory factor
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/product= immediate early protein
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                                                                                                                                                                                                                                                                                                                                                                                                                        /product = capsid protein IV complement (123808..127296)
                                                                                                                                                                                                                                                                                                                                                          complement (111931..112443)
                                                                                                                                                                                                                /product= glycoprotein X complement (93636..94127)
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                                    89600..90541
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96US-0686349.
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96US-0708678
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81 open reading frames
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13-NOV-1996
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                                                                                                                         Best Local Similarity 47.0 Matches 116; Conservative
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                                                                                                               Query Match
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                                                                                                                                            906
                                                                                                  787 AACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCC 846
                                                          727 GGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCTTTGCT 786
                                                                                                                                                                                                                                                                                                                                                                                Spinocerebellar ataxia type III; SCAIII; reverse dot hybridisation; PCR-microplate hybridisation; PCR-MPH; trinucleotide repeat; TNR;
                                                                                                                                          847 AACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACT
                                                                                                                                                                                  907 CCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACTGCTGCT
                  Length 137507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            syndrome
                                       ;
                                       Indels
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using techniques which ensure highly accurate diagnosis
                                                                                                                                                                                                                                                                                                                                                              Spinocerebellar ataxia type III (SCAIII) gene fragment.
                                      0; Mismatches 127;
                   DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= b
/note= "trinucleotide repeat"
                  Score 39.8; DI
Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
137..355
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(SMSU ) SAMSUNG FINE CHEM CO LTD.
                3.18;
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137..139
                          Best Local Similarity 47.7
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    SCAIII syndrome; ss.
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                                                                                                                                                                                                                                             Db 125382 cat 125384
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                   Query Match
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SCAIII gene containing 73 copies of the trinucleotide (CAG) repeat unit (the present sequence) to a substrate, and hybridising with amplified testee genomic DNA containing copies of the trinucleotide units, PCR amplified with labeled primers (X8989-90). The new method is useful for diagnosis of SCAIII syndrome, and for determining the severity of the disease. The present sequence represents the SCAIII gene fragment containing 73 trinucleotide (TNR) repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              846 CAACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            906 rccrarggagarggrcrrcgrgrrgcrggaaccgrrgagrrcgcrggrcrcacrgcrgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                     Length 397;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                          Sequence 397 BP; 124 A; 104 C; 104 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                        DB 20;
                                                                                                                                                                                                                                                                                                                                                     Score 37.4; DB Pred. No. 0.084;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of a murine OPA gene.
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Ginns EI;

Philibert RA,

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gene. The human OPA gene is derived from the PCTG4 region of chromosome xq13. Polymorphisms in this region are associated with mental retardation, autism, depression, bipolar affective disorder or hypothyroidism. One 12 bp insertion polymorphism occurs within the coding region of the human OPA gene, and introduces a 4 amino acid insertion in a putative OPA domain. This domain has been shown to be involved in tissue specific expression. Another polymorphism consists of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp polymorphism. Another polymorphisms consists of a dinucleotide repeat approximately 4.5 kb downstream of the 12 bp polymorphism. Another polymorphisms consists of a dinucleotide repeat specification describes a method for screening for polymorphisms in a PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related sequences within the q13 region of the X chromosome have polymorphisms associated with neuropsychiatric disorders. The methods can be used to screen for the presence of a heritably linked form of mental the chromosial.
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mental retardation; autism; depression; bipolar affective disorder;
hypothyroidism; OPA gene; neuropsychiatric disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           785 CTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCG
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                                                                                                                                                                                                                                                                                                                                                                                           DB 21; Length 6558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      905 CTCCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGT 954
                                                                                                                                                                                                                                                                                                                                    Sequence 6558 BP; 1637 A; 1801 C; 1644 G; 1475 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 2.7%; Score 35.6; Db 21, Best Local Similarity 45.2%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (USSH ) US DEPT HEALTH & HUMAN SERVICES. (IOWA ) UNIV IOWA RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA sequence of human OPA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Z45597 standard; cDNA; 6794 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0083465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                    hypothyroidism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-APR-1998;
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The present sequence represents the CDNA sequence of the human OPA gene, which is derived from the human PCTG4 region of chromosome Xq13. Polymorphisms in this region are associated with mental retardation, autism, depression, bipolar affective disorder or hypothyroidism.

Cone 12 bp insertion polymorphism occurs within the coding region of the human OPA gene, and introduces a 4 amino acid insertion in a putative OPA domain. This domain has been shown to be involved in tissue specific expression. Another polymorphism consists of a pentanucleotide repeat approximately 7 kb upstream of the 12 bp polymorphism. Another polymorphisms consists of a dinucleotide repeat approximately 4.5 kb downstream of the 12 bp polymorphisms. The specification describes a method for screening for polymorphisms in a PCTG4 nucleic acid sequence obtained from a subject. The PCTG4 related sequences within the q13 region of the X chromosome have polymorphisms associated with the research of the X chromosome have polymorphisms associated with presence of a heritably linked form of mental retardation, autism, certain affective disorders or hypothyroidism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        643 GCTAACGGTGGAGAGTTCGTGTCTGCTCGTGTTATCGGATTCGAGACTGAAGGTCGTGCT 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           703 CTCAAGGGTATCACCACCACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coleoptera; transgenic plant; malze; Zea mays; insect resistance; VIP1; Bacillus cereus; western corn rootworm; Diabrotica vergifera vergifera; ss.
                                                                   Identification of polymorphisms in the PCTG4 region of Xq13 for diagnosing mental retardation or autism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pesticide; insecticide; biological control agent; Lepidoptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 6794;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6794 BP; 1624 A; 1938 C; 1754 G; 1478 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.7%; Score 35.2; DB 21; Best Local Similarity 54.7%; Pred. No. 1.7; Matches 70; Conservative 0; Mismatches 58;
                                                                                                                            Example 7; Page 68-71; 100pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Maize-optimized VIP1A(a) gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T13952 standard; DNA; 2004 BP.
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94US-0314594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-AUG-1996 (first entry)
                                 WPI; 2000-126357/11.
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T13952/c
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(CIBA) CIBA GEIGY AG.

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A synthetic gene (T13952) comprises a version of the Bacillus cereus strain AB78 80-kDa VIPIA(a) gene (see also T13941) with codon usage optimised for expression in maize. The synthetic gene encodes VIPIA(a) (R91240), an insect-specific protein showing activity against western corn rootworm. VIPIA(a) can be expressed in transgenic maize to protect the plant from insect attack.
                                                                                                                             Bacillus strain producing insecticidal protein during vegetative growth - used in the control of Lepidoptera and Coleoptera pests % \left( \frac{1}{2}\right) =0
                                       Kostichka K;
                                                                                                                                                                                                                                                                                                                                                                             Sequence 2004 BP; 586 A; 659 C; 530 G; 229 T; 0 other;
                                   sai NM, Duck NB, Estruch JJ,
Mullinsma, Nye GJ, Warren GW;
                                                                                                                                                                                     Claim 48; Page 136-138; 242pp; English.
                                                                                         WPI; 1996-200921/20
                                     Desai NM,
                                                        Koziel MG,
                                     Carr B,
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ö 1426 ACTGGGTGTTCTTCTCGCTCTTCATGTACAGGCTGATGTAGTAGTCGCGGTTCTTCTTCA 1367 915 GATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGTCTCACTGCTCCTAACTG 974 1306 GCTTCTTGCCGTTGTTGCCGCCTCACGATGTTGGTGTTGGTCACTTGCCGATGCTG 1248 795 TGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCCAACCCAGA 854 855 AGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACTCCTATGGA 914 735 TGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCTTCTTGCTAACTCCCT 794 ; 0 Query Match 2.7%; Score 35; DB 17; Length 2004; Best Local Similarity 44.8%; Pred. No. 1; Matches 134; Conservative 0; Mismatches 165; Indels á g g

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Search completed: January 1, 2001, 03:45:17 Job time: 20325 sec

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Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1.;
US-08-770-379-20
US-08-471-033-18
US-08-471-04-18
US-08-471-046-18
US-08-470-566-18
US-08-469-33-18
US-08-471-033-35
US-08-471-044-35
US-08-471-044-35
US-08-471-048-35
US-08-471-048-35
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US-08-471-033-26
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Pred. No. 0;
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REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-391-339-8; Sequence 8, Application US/08391339; Patent No. 5463175; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA (synthetic)
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NAME: Hoerner, Dennis R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1296 base pairs
   double
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Best Local Similarity
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                                                                                                                                                                                                                        1 ATGCCTGAGAACCACAAGAA.......AAACTGGTCCTGCATCCTAA 1296
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Sequence 8, A
Sequence 17,
Sequence 17,
Sequence 7, A
Sequence 6, A
Sequence 6, A
Sequence 17,
Sequence 17,
Sequence 17,
Sequence 17,
Sequence 18,
Sequence 21,
                                                                                                                     Search time 157.96 Seconds
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/5C_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/SC_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-08-484-274A-8

US-08-391-339-17

US-08-391-339-7

US-08-391-339-6

US-08-484-274A-7

US-08-391-339-6

US-08-484-274A-6

US-08-484-274A-3

US-08-391-339-3

US-08-484-274A-4

US-08-391-339-3

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US-08-391-339-33

US-08-484-274A-33

US-08-391-339-33

US-08-484-274A-33

US-08-391-339-32

US-08-391-339-32

US-08-391-339-31

US-08-391-339-28

US-08-391-339-28

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US-08-391-339-28

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US-08-391-339-28

US-08-391-339-28
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                   GenCore version
Copyright (c) 1993 - 2000
                                                                                                                     January 1, 2001, 03:18:19
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB
                                                                                   OM nucleic
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                                                                                                                     Run on:
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ATCCCAGATTCCCTTCCAGTGATTGGTCGTGCTACCCGTACTCCAGACGTTATCTACGCT
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                                                                                                                                                                             Sequence 8, Application US/08484274A Patent No. 5776760 GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (synthetic)
                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION TELEPHONE: (713)789-2679
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100.0%;
                                                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 1296; Conservative
                                                                                                                                                                                                                                                                                             ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                Texas
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                                                                                                                                                                     US-08-484-274A-8
                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBI130 38-21(13560)A
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                  1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                                                                                                                                                                                                                                                                                            700 Chesterfield Village Parkway
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ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA
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                                                                                                                                                                                                                                                                          ADDRESSEE: Dennis R. Hoerner, Jr.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/717,370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   us/08/391,339
                                                                                                                        Sequence 17, Application US/08391339 Patent No. 5463175 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Hoerner, Dennis R., Jr. RECISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-7
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                               BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (314)537-6099 INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
                                                                                                                                                                                                                                                                                               Monsanto Co.
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STRANDEDNESS: double
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MEDIUM TYPE: Floppy
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CITY: St. Louis
STATE: Missouri
COUNTRY: USA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,274A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT130 38-21(13560)A
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1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
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                                                                                                                                                      APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
ATTLE OF INVENTION: Glyphosate Tolerant
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                             Sequence 17, Application US/08484274A Patent No. 5776760
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TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
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99.6%;
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nucleic acid
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Best Local Similarity 99.6
Matches 1291; Conservative
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MEDIUM TYPE: Floppy
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                                                                                                                                   GENERAL INFORMATION:
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ZIP: 77210-4433
                                                                                                                                                                                                                                                                       STREET: P.O. I CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
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US-08-484-274A-17
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Patent No. 5463175
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US-08-391-339-7
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              TITLE OF INVENTIÓN: Glyphosate Tolerant Plants NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                              Version
                                                                ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Mosanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.0%; Score 1011.2;
86.3%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/391,339
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
APPLICATION NUMBER: US/07/717,370
FILING DATE:
                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (recombinant)
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: Hoerner, Dennis R.
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LENGTH: 1296 base pairs
Barry, Gerard
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Matches 1118; Conservative
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                                                 CORRESPONDENCE ADDRESS:
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APPLICANT: Kishore, Ganesh

GENERAL INFORMATION:

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                                                           CCTAACTTGTCTCACGCCTTTACCAAGGGAATCCTTATCGAAGAGAACGGTCACACCATC
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S: Arnold, White & Durkee P.O. Box 4433

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                                                                                                                             APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
ATTONINEY/AGENT INFORMATION:
NAME: PAETERSON, Melinda L.
REGISTRATION NUMBER: 33,062
REGISTRATION NUMBER: 33,062
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ 1D NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1011.2;
Pred. No. 0;
0; Mismatches
                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (recombinant)
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86.3%;
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LENGTH: 1296 base pairs
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Best Local Similarity 86.3
Matches 1118; Conservative
                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                     double
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: doub
                                                                        COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                     linear
         COUNTRY: USA
ZIP: 77210-4433
Texas
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                  AATCCGCAAGGGCTCGTGACCCTCTTGTTTCGGCGTTTTATCGCGGAAGGGTGGCGAATTT
                                      GTGTCTGCTCGTGTTATCGGATTCGAGACTGAAGGTCGTGCTCTCAAGGGTATCACCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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STRETT: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
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Patent No. 5463175
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0; Mismatches 209;
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Pred. No. 0;
                                                                                                                                            38-21(10533)
                                           US/08/156,968
                                                                    US/07/717,370
                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (recombinant) US-08-391-339-6
                                                                                                             NAME: Hoerner, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                74.2%; 83.9%; E
                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner, Dennis R.,
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FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
                                           APPLICATION NUMBER:
                                                       FILING DATE: APPLICATION NUMBER:
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                                     GCTACTCCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT
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                          ACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGTTGCAGCTGGTGCACACTCCAAGTCT
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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FILING DATE: 07 June 1996
CLASSIFICATION: 435
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tole
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
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NAME: Petterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MO
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-484-274A-6
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                                                                                                                                                                  Length 1296;
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                                                                                                                                                                 DB 2;
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0; Mismatches 209;
                                                                                                                                                                 Score 961.6;
                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (recombinant)
US-08-484-274A-6
                                                                                                                                                               74.2%;
83.9%;
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ 1D NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1296 base pairs
                                                                                                                                                                               Best Local Similarity 83.9 Matches 1087; Conservative
                                                         TYPE: nucleic acid
STRANDEDNESS: double
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                                                ATCGCGAATCCGGAAGCCGCTCCACGCATTCCGACGACGATGCGTCAGGAAAATTCATC
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                                GCTACTCCTATGGAGATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/484,274A
FILING DATE: 07 June 1996
CLASSIFICATION: 435
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
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NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: MOBT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 3:
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STRANDEDNESS: double
TOPOLOGY: linear
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ZIP: 77210-4433
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
                                                                                                                                                                                                                      1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
STATE: Missouri
COUNTRY: USA
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83.8%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/391,339 FILING DATE: CASSIFICATION: 800 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/156,968 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/717,370 FILING DATE:
                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: HOEFDE, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFERENCE, DOCKET NUMBER: 38-2.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STRANDEDNESS: double
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Matches 1086; Conserv
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; LOCATION:
US-08-391-339-4
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                                      ATGCCAGGAAACTTGACTAGCGTTCCAAAGTGGCTTCTTGACCCAATGGGTCCATTGTCC
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NAME: Patterson, Melinda L.
REGISTRATION NUMBER: 33,062
REFERENCE/DOCKET NUMBER: M62130 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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); Mismatches 207;
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                                                                                                                                                                                                                                                         APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                  APTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/484,274A FILING DATE: 07 June 1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433 CITY: Houston STATE: Texas
                                                                                                                                                                                                                        Sequence 4, Application US/08484274A Patent No. 5776760
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIble
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83.88;
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 83.8
Matches 1086; Conservative
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US-08-484-274A-4
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                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Date: Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 71.7%; Score 928.8; DB 1; Best Local Similarity 83.8%; Pred. No. 0; Matches 1086; Conservative 0; Mismatches 207;
                                                                                                                                    APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                   1258 ATTGGCAAATCCAAGCAAACGGGTCCGGCAAGTTAA 1293
                     1261 ATTGGTAAGTCCAAGCAAACTGGTCCTGCATCCTAA 1296
                                                                                                                                                                                              ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: Hoernor, Dennis R., Jr.
REGISTRATION NUMBER: 30,914
REFRENCE/DOCKET NUMBER: 38-21(10533)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314,537-609)
INFORMATION FOR SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1689 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
PPLING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/717,370 FILING DATE:
                                                                                                   Sequence 3, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
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ZIP: 63198
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CTTGCTAACTCCCTTGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTG
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Score 58.8; DB 2;
Pred. No. 1.6e-10;
0; Mismatches 2;
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Patent No. 5463175
GENERAL INFORMATION
APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Monsanto co. por. STREET: 700 Chesterfield Village Parkway
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FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
FILING DATE:
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                                                                                                                                          PC-DOS/MS-DOS
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US-08-484-274A-27
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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Best Local Similarity 96.8%;
Matches 60; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                    OPERATING SYSTEM:
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                                COUNTRY: USA
ZIP: 77210-4433
Houston
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Patent No. 5776760
GENERAL INFORMATION:
APPLICANT: Barry, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Annold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/391,339
                                                                                                              APPLICANT: Kishore, Ganesh M.
APPLICANT: Barry, Gerard F.
TITLE OF INVENTION: Glyphosate Tolerant Plants
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr.,
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38-21(10533)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/156,968
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER: 30,914
REPERENCE/DOCKET NUMBER: 38-21(1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                                      Sequence 27, Application US/08391339
Patent No. 5463175
GENERAL INFORMATION:
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Best Local Similarity 96.8 Matches 60; Conservative
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STRANDEDNESS: single
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CITY: St. Louis
STATE: Missouri
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Gaps 30 CGCTGGAGCTGGAATCGTTGGTGTTTGCACTGCTTTGATGCTTCAACGTCGTGGATTCAA 89 ö Length 62; Indels CLAME: PACKETION: 4.2.
ATORNEY/AGENTION: MALINGA L.
NAME: PACKETION NUMBER: 33,062
REGISTRATION NUMBER: 33,062
REGISTRATION NUMBER: MOBILI30 38-21(13560)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713)789-2679
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 62 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/484,274A FILING DATE: U7 June 1996 CLASSIFICATION: 435 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

Search completed: January 1, 2001, 03:18:40 Job time: 29344 sec

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January 1, 2001, 01:12:53 ; Search time 3327.86 Seconds (without alignments) 2407.829 Million cell updates/sec
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                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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117: 9b-9ss18:*
118: 9b-9ss19:*
119: em_9ss13:*
120: 9b-9ss20:*
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123: 9b-9ss21:*
124: 9b-9ss24:*
125: em_9ss14:*
126: em_9ss15:*
127: em_9ss16:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	101111111111111111111111111111111111111	ac06c04.	ba	AL243904 Terraodon AL304427 Tetraodon	C.		-	860 Drosop	Ω	ALISSO/4 TELLACOCII	AL107204 Drosophil	AV182303 AV182303	F.rubripe	σ,	AL338180 Tetraodon	EST3254	AI012527 EST206978	WOV 3 MCA	WOV 3MCA	AIII3539 GH09871.5	AA695185 GM02371 5	AW651210 EST329664	RPCI-23	Leish	vu20e	RR5066 vo40h12 r1	6 SWOV3	3	AW443546 EST308476	AI388163 GH18971.5	AL-108276 Drosophil	0.00	56682 н	96 vx37a04	4 df45e04	24 A	AL285089 Tetraodon	216	3 au55h01.
SUMMARIES DB ID	3 :	2. A	32 B	123 CNSO3H6V	124	124 FR001371	123 CNS04QU	121	, A	122 8 AI	121	16	124	10	124 CNSUSHXN 2 AA250789	23	8 AI01252	5 AA67051	s o	8 AIII353	2 40	23 AW65121	115	124 P149R	9	0 0	10 AI43681	90 AQ24681	25	TO ALSBEID	121 CNS017	123	88 AQ06668	11 AIS5109	50 AW02288	4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	٦ ،	3 BE02491	AI87920
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ALIGNMENTS

RESULT 2 BE019568/c

EMERENCE EMERINGE HORSON EMERENCE 1 (Dases 1 to 482) AUTHORS (Liberia: Primates; Catarrinin; Hominidae; Homo. Indees to 482) AUTHORS (Liberia: Allen, M., Bowles: L., Dubuque, T., Gelsel, G., Jost.S., Milte, L., Allen, M., Bowles: L., Dubuque, T., Gelsel, G., Jost.S., Milte, T., Wable, M., Marti, J., Warte, M., Marti, J., Warte, M., Warti, M., Marti, J., Warte, M., Marti, J., Walle, T., Waterston, R. and Wilson, R. Tan, F., Theising, B., White, Y., Waterston, R. and Wilson, R., Tan, F., Theising, B., White, Y., Waterston, R. and Wilson, R., Tan, F., Theising, B., Till J. (Concer: Wallson ME Parkway, Box 8501, St. Louis, MO 63108 Twashington University School of Madicine Adad Procest Park Parkway, Box 8501, St. Louis, MO 63108 Twas 131 286 1800 Fax: 131 280
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/db_xref="taxon:9606"
/clone_lib="MIH_MGC_21"
/clone_lib="MIH_MGC_21"
/tissue_type="choriocarcinoma"
/lab_host="MIH_MGC_21"
/note="Organ: placenta; vector: pOTB7; Site_l: XhoI;
/note="Organ: placenta; vector: 
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Cen
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Image.llnl.gov/image/html/iresources.shtml
Seq primer: -40RP from Gibco
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NIH-MGC http://www.ncbl.nlm.nih.gov/MGC/.
National Institutes of Health, Mammallan Gene Collection (MGC)
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BE019568 526 bp mRNA EST 06-JUN-2000 ba83f05.yl NIH_MGC_21 Homo sapiens cDNA clone IMAGE:2907009 5'similar to TR:015413 015413 CTG7A ;, mRNA sequence.
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Pred. No. 0.024;
0; Mismatches 124; Indels 0
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -40RP from Gibco
High quality sequence stop: 463.
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BE019568.1 GI:8279646
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Submitted (12-ARR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Dasilva, C., Fizames, C., Fisher, C.,
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                                                          from Tetraodon nigroviridis, genomic survey
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2; Mismatches 176; Indels
                             nigroviridis genome survey sequence T7
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/clone="026011"
/clone_1b="G"
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Tetraodon nigroviridis
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequenching project of the Tetracdon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracdon.
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                                                                                                                  Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 005C20 of library H from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygil; Neopterygil; Teleostei; Euteleostei; Neoteleostei
Eurypterygil; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
                                                                                                                                                                                                                                                                                                                                                                                          Fisher, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the
                                                                                                                                                                                                                                                                                                                            Holacanthopterygli, Acanthopterygli, Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon.
1 (bases 1 to 805)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.
Bouneau, L., Bilault, A., Quetier, F., Saurin, W., Bernot, A. and Welssenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              643 GCTAACGGTGGAGGTTCGTGTCTGCTCGTGTTATCGGATTCGAGACTGAAGGTCGTGCT 702
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/db_xref"taxon:99883"
/clone="005C20"
/clone="105E4"
/note="Genoscope sequence ID : COBH
PUC-ori"
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417 GTTGTTGCTGCTGCTGTTGTTGCT 391
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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Submitted (18-FEB-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 ISB. Email: biohelp@hgmp.mrc.ac.uk
Vector: pBluescript II KS
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clone 133B16aC7, genomic survey sequence.
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942
                                              639 GCTGCTGGTGCTGCTGCTGCTGCTGCTACTGGTGCTGCTGCTGGTGGTGCT 698
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Pred. No. 0.1;
0; Mismatches 176;
                                                                                                    943 GAGTTCGCTGGTCTCACTGCTGCTAACTGGAAGCGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Fugu rubripes"
/db_xref="taxon.31033"
/clone_lib="cosmid 133B16"
/clone="133B16a7"
150 c 116 g 175 t
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llarity 45.0%;
Conservative
                                                                                                                                                                                                                                                                                                   619 bp
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
                     Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
                                                                                                                                                                                                                                            Costs: 1 to 1003)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Meroet-Crollius, H., Jaillon, O., Dasilva, C., Bouteiler, F., Brames, C., Wincker, P., Brottier, P., Quetler, F., Burin, W. and Melssenbach, J. Human gene number estimate provided by genome wide analysis using Unpublished
Unpublished
1 (bases 1 to 1003)
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR07E07 of RPCI-98 library from Drosophila melanogaster (fruit
    Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                           Holacanthopterygil; Acanthopterygil; Percomorpha; Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Tetraodon. 1 (bases 1 to 1003)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="130A16"
/clone_lib="G"
/note="Genoscope sequence ID : C0B
296 c 282 g 234 t 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40.4; DB 123;
Pred. No. 0.53;
0; Mismatches 136;
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Best Local Similarity 47.3%;
Matches 122; Conservative 0
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                     s 18-SEP-1997
genomic survey sequence.
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Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Percomorpha;
Tetraodontiformas; Tetraodontoidei; Tetraodontidae; Fugu.
1 (bases 1 to 619)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 ISB. Email: biohelp@hgmp.mrc.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               842 TCGCCAACCCAGAAGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCG 901
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                                        clone 133B16dB11,
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43.3%; Pred. No. 0.39;
tive 0; Mismatches 182;
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/db_xref="taxon:31033"
/clone_lib="cosmid 133B16"
/clone="133B16dB11"
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Tetracdon nigroviridis.
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Fugu rubripes
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/note-"Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2: XhoI; Sized fractionated cDNAs were directly ligated into
                                                                                                                                                             Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Maccomchab; Ephydroldea; Drosophilidae; Drosophila. [ (bases 1 to 752) Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M. [BDGP/HHMI Drosophila EST Project [Unpublished (1997)]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei Eurypterygii; Ctenosquamatei Acanthomorpha; Euracanthomorpha; Holacanthopterygii; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontcidel; Tetraodontidae; Tetraodon.
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Tetraodon nigroviridis genome survey sequence T7 end of clone
141F22 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Harvey. D.
Contact: Harvey. D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Fax: 510 643 9947
Fax: 510 tow: B column: 1
High quality sequence stop: 639.
Location/Qualifiers
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher,
Boureau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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//db_xref="texon:727"
//clone="LD23113"
//clone_lib="LD Drosophila melanogaster embryo pOT2"
//csex="male and female"
//dev_stage="0" to 24" hours mixed stage embryonic"
/lab_nost="XLI Blue"
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                                                                                                                                                                                                                           Direct Submission

Submitted (10-21W-1999) Genoscope - Centre National de Sequencage:

By 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr
- Gollaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDCP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDCP Drosophila
melanogaster BAC ilbrary was prepared by Kazutoyo Oscegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Fark Cancer Cittute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
ECORI digestion of Drosophila DNA provided by the BDCP from the
isogenic strain v2s: on bw sp, the same strain used for the BDGP's
pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library or
fillters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ptertygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1. (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR07E07"
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Pred. No. 0.55;
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306 c 227 g
Drosophila melanogaster
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                                                                                                                                                                                                     Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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                                              Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetler, F., Saurin, W. and Weissenbach, T. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choi.W., Fang, E., Sasinowski, M., Wing, R. and Dean, R.A.
Spressed sequence characterization during appressorium formation
in rice blast fungus, Magnaporthe grisea
Unpublished (1998)
                                                                                                                                                                                                                                                                                           Location/Qualifiers

1. .906

/organism Tetraodon nigroviridis"
/db_xref "taxon:99883"
/clone "141F22"
/clone "Genoscope sequence ID : COAG141DC11LP1-end : T7"
/note "Genoscope sequence ID : COAG141DC11LP1-end : T7"
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Magnaporthaceae; anamorphic Magnaporthaceae; Pyricularia
1 (bases 1 to 946)
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freshwater pufferfish Tetraodon nigroviridis
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Pred. No. 0.68;
1; Mismatches 131;
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Clemson University Genomics Institute
Clemson University
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Pyricularia grisea
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                              Jobes Wector: pBlueScriptII SK(+) Vector; Site_1: EcoRI; Site_2: XhoI; The appressorium formation-specific cDNA library was constructed form conidia germinated for 5-8 hr on an inductive surface. The library has an average insert size of 1.5 kbp. 3 others
                                                                                                                                                                                                                                                                                                                                 /dev_stage="Germinated conidia on appressor!um-inductive surface"
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                                                                                                                                                                                                                                                                         /clone="mgae0006cc09f"
/clone_lib="Magnaporthe grisea Appressorium Stage cDNA
Library"
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Muscomorpha, Ephydroidea, Drosophilidae, Drosophila,
1 (bases 1 to 1101)
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47.7%; Pred. No. 0.79;
ive 0; Mismatches 127; Indels
100 Jordan Hall, Clemson University, Clemson, Tel: 864 656 5737
Email: rdean@clemson.edu
Seq primer: T3 primer (AATTAACCGTCACTAAAGGG)
High quality sequence stop: 403.
Locatlon/Qualiflers
1. 946 (Mountain AATTAACCGTCACTAAAGGG)
                                                                                                                                                                                                    /organism="Pyricularia grisea"
/strain="70-15"
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Contact: Yuji Kohara
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Matches 105; Conservative
                     Gene Library Lab
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV182303 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite embryo Caenorhabditis elegans cDNA clone yk633h6 3', mRNA sequence. AV182303
library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBACII.
                                                                                                                                                                                                                                                                                                                                                       GTCGTCTCAACGGTGTTCGTACTCAAATCCTCAGCGCTGATGCATTGCGTGATTTCGATC 541
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                                                                                              / ...1101
/organid="Drosophila melanogaster"
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9 a 71 c 171 g 226 t 454 ot
                                                                                                                                                                                                                                                                                   Best Local Similarity 22.0%; Pred. No. 1.1;
Matches 94; Conservative 134; Mismatches 199;
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AV182303 Yuji Kohara
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Fugur Tubripes
Budraryota; Metacoa; Chordata; Vertebrata; Actinopterygil;
Neopterygil; Teleostei; Euteleostei; Acanthopterygil; Percomorpha;
Tetraodontiformes; Tetraodontoidei; Tetraodontidae; Fugu.
(pases l to 567)
Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
Submitsed (18-FEB-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F.rubripes GSS sequence, clone 133B16bB5, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                599 TCAACCCACAAGGTCTCGTGACTCTTTTTTTCGTCGTTTTCATCGCTAACGGTGGAGAGT 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    659 TCGTGTCTCCTCGTGTTATCGGATTCGAGCTGAAGGTCGTGCTCTCAAGGGTATCACCA 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  719 CCACCAACGGTGTTCTTGCTGTTGATGCAGCTGTTGCTGCTGGTGCACCACCACCAAGT 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.0%; Score 39; DB 16; Length 300; 48.6%; Pred. No. 0.93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 111; Indels
                                                                                                                                                               /organism="Caenorhabditis elegans"/strain="N2"
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tal: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
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/organism="Fugu rubripes"
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/clone_1ib="cosmid 133B16"
/clone="133B16bB5"
a 156 c 123 g 171 t
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/clone_lib-"Yuji Kohara ur
hermaphrodite embryo"
/sex="hermaphrodite"
/dev_stage="embryo"
a 59 c 86 g 103
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BDGP/HHMI Drosophila EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                 AI402856 612 bp mRNA EST 08-FEB-1999 GH22177.5prime GH Drosophila melanogaster head pOT2 brosophila melanogaster cDNA clone GH22177 5prime similar to M23221: fs(1)h FBgn0004656 PID:9157453 SWISS-PROT:P13709, mRNA sequence.
                                                     TGGTGATGACATCCCATTGGATACCGAACGTGGATACCACATCGTGATCGCCAACCCAGA 854
                                                                                                                                           141 TACTGCTGCTACTANNGNTGCTGCTANTGCTGNTGCTGCTGCTGCTGCTGCTAC 200
                                                                                                                                                                         855 AGCTGCTCCACGTATTCCAACTACCGATGCTTCTGGAAAGTTCATCGCTACTCCTATGGA 914
                                                                                                                                                                                            915 GATGGGTCTTCGTGTTGCTGGAACCGTTGAGTTCGCTGGTCTCACTGCTGCTGCTAACTG 974
                                                                                                                                                                                                                                                    261 TGCTACTGCTGCTGCTGCTGCTGCTGCTACTACTACTACTACTGCTGCTGCTGCTAC
                                        Gaps
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                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroldea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
Plate: 221 row: G column: 5
High quality sequence stop: 573.
Location/Qualifiers
   Score 39; DB 124; Length 5
Pred. No. 1.1;
0; Mismatches 167; Indels
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G. M. Rubhn-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
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AIÁ02856.1 GI:4245943
3.0%;
              Best Local Similarity 44.19
Matches 132; Conservative
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Query Match
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       Gaps
                           CTGGTGCACACTCCAAGTCTCTTGCTAACTCCCTTGGTGATGACATCCCATTGGATAC 818
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     Indels
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 Conservative
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Search completed: January 1, 2001, 01:13:01 Job time: 25800 sec

Ouery Match 3.0%; Score 38.8; DB 10; Length 612; Best Local Similarity 51.1%; Pred. No. 1.3;